

OM protein - protein search, using sw model

Run on: November 11, 2002, 11:40:16 ; search time 62 Seconds (without alignments)
184.832 Million cell updates/sec

Title: PCT-US02-27855-1
Perfect score: 499
Sequence: 1 KTCYEGNGHFYRGKASTDM. YVQVGLKPLVQECMVHDCAD 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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A_Geneseq_101002:*
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2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	494	99.0	88	23	AAE16542	Human urokinase-type Human urokinase-kringle
2	494	99.0	96	23	AAE16550	Human urokinase-type Human urokinase-aminopeptidase
3	494	99.0	135	23	AAE16545	Human urokinase-type Human urokinase-aminopeptidase
4	494	99.0	143	23	AAE16549	Human urokinase-type Human urokinase-aminopeptidase
5	494	99.0	337	22	AAG75492	Human urokinase-type Human urokinase-aminopeptidase
6	494	99.0	337	23	ABP41795	Human ovarian anti-urokinase antibody
7	494	99.0	365	16	AAR68854	Human ovarian anti-urokinase antibody
8	494	99.0	378	11	AAW13635	Human prourokinase
9	494	99.0	386	16	AAR66266	Bifunctional urokinase
10	494	99.0	389	11	AAW13636	Human prourokinase

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OM protein - protein search, using sw model

Run on: November 11, 2002, 11:40:16 ; Search time 62 seconds
 (without alignments)
 184.832 Million cell updates/sec

Title: PCT-US02-27855-1

Perfect score: 499

Sequence: 1 KTCYEGNGHFYRGKASSTDM. YVQVGLKPLVQECMVHDCAD 86

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

11 ALIGMENTS

XX
PT Composition for modulating muscle cell and tissue contractility for
PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
PT comprising domains from urokinase-type plasminogen activator -
XX
PS Claim 1; FIG 1A; 117pp; English.

The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation, and a disorder sequence is human urokinase-type plasminogen activator (uPA) kringle.

XX
SQ Sequence 88 AA;

Query Match 99.0%; Score 494; DB 23; Length 88;

Best Local Similarity 98.8%; Pred. No. 1.8e-41; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGKHNCRNPDN 60
Db 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSDALQLGKHNCRNPDN 60
Qy "61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

RESULT 2

AAE16550
ID AAE16550 standard; Protein; 96 AA.
XX
AC AAE16550;
XX
DT 09-APR-2002 (first entry)

DE Human uPA kringle and connecting peptide.
XX
KW Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
KW stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
KW microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
KW tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
KW clotting disorder; uterine contraction disorder; respiratory disease;
KW adult respiratory distress syndrome; male impotence.

XX
OS Homo sapiens.
XX
PN WO200197752-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US18976.
XX
PR 20-JUN-2000; 2000US-212874P.
XX
(UYPE-) UNIV PENNSYLVANIA.
XX
PA Cines DB, Higazi AA;
XX
DR WPI; 2002-122240/16.
XX
DR N-PSDB; AAD27083.

XX
PT comprising domains from urokinase-type plasminogen activator -
XX
PS Claim 25; FIG 1I; 117pp; English.

The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) kringle and connecting peptide.

XX
SQ Sequence 96 AA;

Query Match 99.0%; Score 494; DB 23; Length 96;

Best Local Similarity 98.8%; Pred. No. 1.9e-41; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGKHNCRNPDN 60
Db 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSDALQLGKHNCRNPDN 60
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

RESULT 3

AAE16545
ID AAE16545 standard; Protein; 135 AA.
XX
AC AAE16545;
XX
DT 09-APR-2002 (first entry)

DE Human urokinase-type plasminogen activator amino terminal fragment (ATF).
XX
KW Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
KW stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
KW microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
KW tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
KW clotting disorder; uterine contraction disorder; respiratory disease;
KW adult respiratory distress syndrome; amino terminal fragment; ATF;
KW male impotence.

XX
OS Homo sapiens.
XX
PN WO200197752-A2.
XX
PD 27-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US18976.
XX
PR 20-JUN-2000; 2000US-212874P.
XX
(UYPE-) UNIV PENNSYLVANIA.
XX
PA Cines DB, Higazi AA;
XX
DR WPI; 2002-122240/16.
XX
DR N-PSDB; AAD27078.

XX
PT composition for modulating muscle cell and tissue contractility for
PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
PT comprising domains from urokinase-type plasminogen activator -

XX
PS Claim 11; Fig 1D; 117pp; English.
XX
CC The invention relates to a composition comprising one or more domains of
CC urokinase-type plasminogen activator (uPA). The composition is used to
CC modulate the contractility and angiogenic activity of a mammalian muscle,
CC endothelial cell or tissue. The composition is used for treating stroke,
CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
CC diabetic retinopathy, wound healing, clotting disorder, uterine
CC contraction disorder, male impotence, respiratory disease or condition
CC such as asthma, adult respiratory distress syndrome, primary pulmonary
CC hypertension, microvascular thrombotic occlusion, and a disorder
CC associated with chronic intrapulmonary fibrin formation. The present
CC sequence is human urokinase-type plasminogen activator (uPA) amino
CC terminal fragment (ATF).
XX
SQ Sequence 135 AA:

Query Match 99.0%; Score 494; DB 23; Length 135;
Best Local Similarity 98.8%; Pred. No. 2.7e-41; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNCRNPDN 60
Db 48 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNCRNPDN 107
QY 61 RRRPWCVYQVGLKPLVQECMVHDCAD 86
Db 108 RRRPWCVYQVGLKPLVQECMVHDCAD 133

XX
PS Claim 24; Fig 1H; 117pp; English.
XX
CC The invention relates to a composition comprising one or more domains of
CC urokinase-type plasminogen activator (uPA). The composition is used to
CC modulate the contractility and angiogenic activity of a mammalian muscle,
CC endothelial cell or tissue. The composition is used for treating stroke,
CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
CC diabetic retinopathy, wound healing, clotting disorder, uterine
CC contraction disorder, male impotence, respiratory disease or condition
CC such as asthma, adult respiratory distress syndrome, primary pulmonary
CC hypertension, microvascular thrombotic occlusion, and a disorder
CC associated with chronic intrapulmonary fibrin formation. The present
CC sequence is human urokinase-type plasminogen activator (uPA) amino
CC terminal fragment (ATF) and connecting peptide.
XX
SQ Sequence 143 AA:

Query Match 99.0%; Score 494; DB 23; Length 143;
Best Local Similarity 98.8%; Pred. No. 2.8e-41; Indels 0; Gaps 0;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNCRNPDN 60
Db 48 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNCRNPDN 107
QY 61 RRRPWCVYQVGLKPLVQECMVHDCAD 86
Db 108 RRRPWCVYQVGLKPLVQECMVHDCAD 133

RESULT 4
AAE16549
ID AAE16549 standard; Protein; 143 AA.
XX
AC AAE16549;
XX
DT 09-APR-2002 (first entry)
XX
DE Human uPA amino terminal fragment (ATF) and connecting peptide.
XX
KW Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
KW stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
KW microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
KW tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
KW clotting disorder; uterine contraction disorder; respiratory disease;
KW adult respiratory distress syndrome; amino terminal fragment; ATF;
KW male impotence.
XX
OS Homo sapiens.
XX
PN WO200197752-A2.
XX
PD 27-DEC-2001.
XX
PP 13-JUN-2001; 2001WO-US18976.
XX
PR 20-JUN-2000; 2000US-212874P.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Cines DB, Higazi AA;
XX
DR WPI; 2002-122240/16.
DR N-PSDB; AAD27082.
XX
PT Composition for modulating muscle cell and tissue contractility for
PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
PT comprising domains from urokinase-type plasminogen activator -
XX

XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX
PT useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 11; Page 7707-7708; 9803pp; English.
XX
AAH32943 to AAH37195 and AAG73514 to AAG7788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene

CC therapy and vaccine production. N and P may be used in the prevention, CC diagnosis and treatment of diseases associated with inappropriate P CC expression. For example, N and P may be used to treat disorders CC associated with decreased expression by rectifying mutations or deletions CC in a patient's genome that affect the activity of P by expressing CC inactive proteins or to supplement the patient's own production of P. CC Additionally, N may be used to produce the colon cancer-associated P's, CC by inserting the nucleic acids into a host cell and culturing the cell CC to express the proteins. N and P can be used in the prevention, diagnosis CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 CC and AB7789 represent sequences used in the exemplification of the CC present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were CC missing at time of publication, meaning no sequences are present for CC SEQ ID NO:1027 to 1052, 7921 and 7922.

XX Sequence 337 AA:

Query Match 99.0%; Score 494; DB 22; Length 337;

Best Local Similarity 98.8%; Pred. No. 6.5e-41;

Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60

Db 74 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 133

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

Db 134 RRRPWCYVQVGLKPLVQECMVHDCAD 159

RESULT 6

ID ABP41795

ID ABP41795 standard; Protein; 337 AA.

XX

AC ABP41795;

DT 22-AUG-2002 (first entry)

DE Human ovarian antigen HWVCB79, SEQ ID NO:2927.

XX

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60

Db 74 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 133

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

Db 134 RRRPWCYVQVGLKPLVQECMVHDCAD 159

RESULT 7

ID AAR68854

ID AAR68854 standard; protein; 365 AA.

XX

AC AAR68854;

XX

PN WO200200677-A1.

XX

PD 03-JAN-2002.

XX

PF 07-JUN-2001; 2001WO-US18569.

XX

PR 07-JUN-2000; 2000US-209467P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;

XX

DR WPI; 2002-147878/19.

XX

DR N-PSDB; ABQ54872.

XX

Isolated nucleic acid molecules encoding novel ovarian polypeptides, PT useful in the prevention, treatment and diagnosis of cancer (e.g. PT ovarian cancer), immune disorders, cardiovascular disorders and PT neurological diseases -

XX

claim 11; SEQ ID NO 2927; 2922pp; English.

PS

XX

The invention relates to 2175 novel human ovarian antigens (ABP41054- CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also CC encompasses polypeptides 90% identical and polynucleotides 95% identical CC to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen CC polynucleotides, antibodies against human ovarian antigens, and the use CC of ovarian antigen polynucleotides and polypeptides in diagnosing, CC treating, prognosing or preventing various ovary and/or breast-related CC disorders. Such conditions include ovarian cancer and breast cancer, and CC metastatic tumours of ovarian or breast origin, reproductive system CC disorders (e.g., infertility, disorders of pregnancy, anovulation, CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic CC shock syndrome), inflammatory conditions (e.g., mastitis, cophoritis and CC vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), CC blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and CC polynucleotides may also be used in screening for compounds which CC further be used for gene therapy, chromosome mapping, in the CC identification of individuals and in forensic analysis, and the CC polypeptides may be used as food additives or to prepare antibodies CC useful in disease diagnosis, drug targeting and phenotyping. The present CC sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp://wipo.int/pub/published_pct_sequences.

XX

Sequence 337 AA:

Query Match 99.0%; Score 494; DB 23; Length 337;

Best Local Similarity 98.8%; Pred. No. 6.5e-41;

Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60

Db 74 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 133

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

Db 134 RRRPWCYVQVGLKPLVQECMVHDCAD 159

RESULT 7

ID AAR68854

ID AAR68854 standard; protein; 365 AA.

XX

AC AAR68854;

XX

PN WO200200677-A1.

XX

PD 03-JAN-2002.

XX

PF 07-JUN-2001; 2001WO-US18569.

XX

PR 07-JUN-2000; 2000US-209467P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Birse CE, Rosen CA;

XX

DR WPI; 2002-147878/19.

XX

DR N-PSDB; ABQ54872.

XX

Isolated nucleic acid molecules encoding novel ovarian polypeptides, PT useful in the prevention, treatment and diagnosis of cancer (e.g. PT ovarian cancer), immune disorders, cardiovascular disorders and PT neurological diseases -

XX

Key Location/Qualifiers

FT Misc-difference 1 /note= "amino acids 1-46 of wild-type urokinase have been deleted"

FT US5376547-A.

XX

PT 27-DEC-1994.

PR 30-JAN-1987; 87US-0008795.
 PF XX
 PR 30-JAN-1987; 87US-0008795.
 PR 29-JAN-1988; 88US-0150267.
 PR XX
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PT Hung PP, Kalyan NK, Lee SL;
 PI XX
 DR WPI; 1995-043464/06.
 PR XX
 PT New modified plasminogen activator cpds. - having regions removed
 to reduce affinity for liver membranes and increase circulation
 PT half-life.
 XX
 PS Claim 1; ; 26pp; English.
 XX
 CC Amino acid residues 1-46 contain the EGF region of human urokinase.
 CC Deletion of this region results in a plasminogen activator with
 CC reduced affinity for liver cell membranes; the mutant protein is
 CC not cleared from the circulation as rapidly as is wild-type tPA.
 CC The specification only gives the sequence around the deletion and
 CC not the full-length sequence of "delta 1-46 urokinase"; the
 CC sequence in AAR68854 has been obtained by amending a previously
 CC disclosed wild-type human urokinase sequence (from WO9501427)
 CC according to the description given in Example 3.
 XX
 SQ sequence 365 AA;
 Query Match 99.0%; Score 494; DB 16; Length 365;
 Best Local Similarity 98.8%; Pred. No. 7e-41; Mismatches 1; Indels 0; Gaps 0;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSNALQGLGKHNHYCRNPDN 60
 ID 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSNALQGLGKHNHYCRNPDN 60
 Db 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87
 RESULT 8
 AAW13635
 ID AAW13635 standard; Protein; 378 AA.
 AC AAW13635;
 XX
 DT 04-JUN-1997 (first entry)
 XX
 DE Human prourokinase variant lacking entire EGF domain.
 XX
 KW Human; prourokinase; hPUK; variant; half-life; increase; EGF;
 KW epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..9
 FT /note= "residues 1-9 of native hPUK"
 FT Region 10..378
 FT /note= "residues 43-411 of native hPUK"
 FT Misc-difference 144
 FT /note= "corresponds to TAC codon"
 XX
 PN EP398361-A.
 XX
 PD 22-NOV-1990.
 XX
 PR 18-MAY-1989; 89JP-0126433.
 PR 03-JUL-1986; 86JP-0156936.
 PR 18-FEB-1987; 87JP-0036495.
 PR 18-MAY-1989; 89JP-0126434.
 PR XX
 PA (GREC) GREEN CROSS CORP.
 XX
 PT Airmura H, Amatsuji Y, Hirose M, Kasai S, Kawabe H;
 PI XX
 DR N-PSDB; AAT61672.
 PR XX
 PT Human pro-urokinase variants - deficient in loop regions of
 PT epidermal growth factor, showing long blood half-life, as
 PT fibrinolytic agent
 XX
 PS Claim 1; Page -; 22pp; English.
 XX
 CC New variants of human prourokinase (hPUK) comprise a hPUK deficient
 CC in (i) at least part of the first loop region of the epidermal growth
 CC factor (EGF) domain; (ii) at least part of the first loop and at
 CC least part of the second loop; or (iii) at least part of the third
 CC loop. The hPUK variants show an increased blood half-life comparable
 CC to that of the whole EGF domain-deficient hPUK variant and urokinase
 CC while retaining the same properties as those of hPUK. They have
 CC potent thrombolytic activity and very little tendency to cause
 CC spontaneous bleeding. The present sequence represents a specific variant
 CC of hPUK which lacks the entire EGF domain; the sequence does not
 CC appear in the specification and has been created using the
 CC wild-type hPUK sequence and the junction sequence after
 CC deletion, both of which are given (in Fig 1 and in Fig 2(3),
 CC respectively).
 XX
 SQ sequence 378 AA;
 Query Match 99.0%; Score 494; DB 11; Length 378;
 Best Local Similarity 98.8%; Pred. No. 7.2e-41; Mismatches 1; Indels 0; Gaps 0;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSNALQGLGKHNHYCRNPDN 60
 ID 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSNALQGLGKHNHYCRNPDN 74
 Db 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 62 RRRPWCYVQVGLKPLVQECMVHDCAD 100
 RESULT 9
 AAR66266
 ID AAR66266 standard; protein; 386 AA.
 AC AAR66266;
 XX
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M33.
 XX
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
 FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159

FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Region 365..366
 FT /note= "peptide bond"
 FT /label= xl
 FT /label= y1
 XX PN DE4323754-C.
 XX PD 01-DEC-1994.
 XX PF 15-JUL-1993; 93DE-4323754.
 XX PR 15-JUL-1993; 93DE-4323754.
 XX PA (CHEF) GRUENTHAL GMBH.
 XX PI Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PI Wnendt S;
 XX DR WPI; 1995-015191/03.
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX PS Example 1; Page 11 and Fig 1; 34pp; German.
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R662666
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thrombolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.
 XX SQ Sequence 386 AA;
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 Best Local Similarity 98.8%; Pred. No. 7.4e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 61
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 Db 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87
 RESULT 10
 AAW13636 ID AAW13636 standard; Protein; 389 AA.
 XX AC AAW13636;
 XX DT 04-JUN-1997 (first entry)
 XX DE Human prourokinase variant lacking EGF domain loops 1 and 2.
 XX Human; prourokinase; hPK; variant; half-life; increase; EGF;
 KW epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
 OS Homo sapiens.
 OS Synthetic.
 XX FH Key
 FT Region 1..10 Location/Qualifiers

FT Region /note= "residues 1-10 of native hPUK"
 FT /note= "residues 33-411 of native hPUK"
 FT Misc-difference 155
 FT /note= "corresponds to TAC codon"
 XX PN EP398361-A.
 XX PD 22-NOV-1990.
 XX PF 18-MAY-1990; 90EP-0109472.
 XX PR 22-FEB-1990; 90JP-0042020.
 PR 18-MAY-1989; 89JP-0126433.
 PR 03-JUL-1986; 86JP-0156936.
 PR 18-FEB-1987; 87JP-0036495.
 PR 18-MAY-1989; 89JP-0126434.
 XX PA (GREC) GREEN CROSS CORP.
 XX PI Airmura H, Amatsuji Y, Hirose M, Kasai S, Kawabe H;
 PI Morita M, Tanabe T;
 XX DR WPI; 1990-350146/47.
 DR N-PSDB; AAT61673.
 XX PT Human pro-urokinase variants - deficient in loop regions of
 PT epidermal growth factor, showing long blood half-life, as
 PT fibrinolytic agent
 XX PS Claim 6; Page -; 22pp; English.
 CC New variants of human prourokinase (hPUK) comprise a hPUK deficient
 CC in (i) at least part of the first loop region of the epidermal growth
 CC factor (EGF) domain; (ii) at least part of the first loop and at
 CC least part of the second loop; or (iii) at least part of the third
 CC loop. The hPUK variants show an increased blood half-life comparable
 CC to that of the whole EGF domain-deficient hPUK variant and urokinase
 CC while retaining the same properties as those of hPUK. They have
 CC potent thrombolytic activity and very little tendency to cause
 CC spontaneous bleeding. The present sequence represents a specific
 CC variant of hPUK which lacks loops 1 and 2 of the EGF domain; the
 CC sequence does not appear in the specification and has been created
 CC using the wild-type hPUK sequence and the junction sequence after
 CC deletion, both of which are given (in Fig 1 and on page 8,
 CC respectively).
 XX SQ Sequence 389 AA;
 Query Match 99.0%; Score 494; DB 11; Length 389;
 Best Local Similarity 98.8%; Pred. No. 7.5e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 60
 Db 26 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 85
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 Db 86 RRRPWCYVQVGLKPLVQECMVHDCAD 111
 RESULT 11
 AAR66245 ID AAR66245 standard; protein; 390 AA.
 XX AC AAR66245;
 XX DT 17-AUG-1995 (first entry)
 XX DE Bifunctional urokinase variant M12.
 XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;

KW urokinase; variant; mutein.
 XX OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 FT Disulfide-bond 4..85
 FT Disulfide-bond 25..67
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Region 366..371
 FT Region /label= x1
 FT Region /label= y1
 FT
 PN DE4323754-C.
 XX
 PD 01-DEC-1994.
 XX
 PR 15-JUL-1993; 93DE-4323754.
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 PA (CHEF) GRUENTHAL GMBH.
 XX
 PT Héinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PT Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thrombolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 XX and pulmonary embolism.
 SQ Sequence 390 AA;
 Query Match 99.0%; Score 494; DB 16; Length 390;
 Best Local Similarity 98.8%; Pred. No. 7.5e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 60
 DB 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 61
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 DB 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87
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 AAR66247
 ID AAR66247 standard; protein; 390 AA.
 XX
 AC AAR66247;
 XX
 KW Bifunctional urokinase variant M14.
 XX DE
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 FT Disulfide-bond 4..85
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 PN DE4323754-C.
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 PR 15-JUL-1993; 93DE-4323754.
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 PA (CHEF) GRUENTHAL GMBH.
 XX
 PT Héinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PT Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thrombolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.
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 SQ Sequence 390 AA;
 Query Match 99.0%; Score 494; DB 16; Length 390;
 Best Local Similarity 98.8%; Pred. No. 7.5e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 60
 DB 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 61
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 DB 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87
 RESULT 13
 AAR66247
 ID AAR66247 standard; protein; 390 AA.
 XX
 AC AAR66247;
 XX
 KW Bifunctional urokinase variant M14.
 XX DE
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..365
 FT /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 FT Disulfide-bond 4..85
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 FT Disulfide-bond 56..80
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 FT Disulfide-bond 143..159
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 PD 01-DEC-1994.
 XX
 PR 15-JUL-1993; 93DE-4323754.
 XX
 PA (CHEF) GRUENTHAL GMBH.
 XX
 PT Héinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PT Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thrombolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.
 XX
 SQ Sequence 390 AA;
 Query Match 99.0%; Score 494; DB 16; Length 390;
 Best Local Similarity 98.8%; Pred. No. 7.5e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 60
 DB 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGKHNVCRNPDN 61

AAR66254
 ID AAR66254 standard; protein: 392 AA.
 XX
 AC AAR66254;
 XX
 DT 17-AUG-1995 (first entry)
 DE Bifunctional urokinase variant M21.
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 KW fibrinolysis; thrombin inhibition; thromolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 FH Key
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 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 PD 01-DEC-1994.
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 PR 15-JUL-1993; 93DE-4323754.
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 PA (CHEF) GRUENTHAL GMBH.
 XX
 PT Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PT Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thromolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.
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 DB 2 KTCYEGNGHFRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQGLGKHNHYCRNPDN 61
 QY 61 RRRPWCVQVGLKPLVQECMVHDCAD 86

Db 62 RRRPWCVQVGLKPLVQECMVHDCAD 87

RESULT 14

AAR66255
 ID AAR66255 standard; protein: 392 AA.
 XX
 AC AAR66255;
 XX
 DT 17-AUG-1995 (first entry)
 DE Bifunctional urokinase variant M22.
 XX
 KW fibrinolysis; thrombin inhibition; thromolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 FH Key
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 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 PA (CHEF) GRUENTHAL GMBH.
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 PT Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PT Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.
 XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR66244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thromolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.
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 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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 Best Local Similarity 98.8%; Pred. No. 7.5e-41;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 60
 Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 61

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 60
 Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSNALQGLGKHNCRNPDN 61

RESULT 15
 AAR6256
 ID AAR6256 standard; protein; 392 AA.
 AC AAR6256;
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 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M23.
 XX
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
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 OS Synthetic.
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 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
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 FT Disulfide-bond 25..67
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 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
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 FT Disulfide-bond 247..316
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 PD 01-DEC-1994.
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 PF 15-JUL-1993; 93DE-4323754.
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 PA (CHEF) GRUENTHAL GMBH.
 XX
 PI Heinzel-Wieland R, Saunders DJ, Schneider J, Steffens GJ;
 PI Wnendt S;
 XX
 DR WPI; 1995-015191/03.
 XX
 PT New bifunctional urokinase derivs and related plasmids - with
 PT improved fibrinolytic and thrombin inhibiting activities, for
 PT treating cardiac and cerebral infarct, pulmonary embolism, etc
 XX
 PS Example 1; Page 10 and Fig 1; 34pp; German.

XX
 CC Bifunctional urokinase derivatives corresponding to the formula
 CC M4-X1-Y1 are claimed (see features table). Sequences AAR6244-R66266
 CC are specific examples of such derivs. which have both improved
 CC fibrinolytic and thrombin-inhibiting activities, compared to known
 CC plasminogen activators or thrombin inhibitors. The proteins are
 CC useful as thrombolytic agents, e.g. for treatment of arterial
 CC occlusions, deep vein thrombosis, cardiac and cerebral infarction
 CC and pulmonary embolism.

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SUMMARIES

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6	494	99.0	403	10	US-09-880-503-6
7	494	99.0	411	10	US-09-880-503-3
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10	216	43.3	562	10	US-09-969-271-7
11	215	43.1	562	9	US-09-974-298-145
12	188.5	37.8	560	10	US-09-912-559-3
13	188.5	37.8	560	10	US-09-912-559-4
14	151	30.3	368	10	US-09-761-120-42
15	149	29.9	378	10	US-09-873-676-1
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ALIGNMENTS

RESULT 1	US-09-880-503-1
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Sequence 2, Appli	Patent No. US20020131964A1
Sequence 3, Appli	GENERAL INFORMATION:
Sequence 4, Appli	APPLICANT: CINES, Douglas B
Sequence 5, Appli	APPLICANT: HIGAZI, Abd Al-Roof
Sequence 6, Appli	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND TISSUE CONTRACTABILITY
Sequence 7, Appli	FILE REFERENCE: 9596-331
Sequence 8, Appli	CURRENT APPLICATION NUMBER: US/09/880, 503
Sequence 9, Appli	CURRENT FILING DATE: 2001-06-13
Sequence 10, Appli	PRIOR APPLICATION NUMBER: US 60/212, 847
Sequence 11, Appli	PRIOR FILING DATE: 2000-06-20
Sequence 12, Appli	NUMBER OF SEQ ID NOS: 18
Sequence 13, Appli	SOFTWARE: PatentIn Ver. 2.1
Sequence 14, Appli	SEQ ID NO 1
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Sequence 25, Appli	Db 61 RRRPWCCYVQVGLKPLVQECMVHDCAD 86
Sequence 26, Appli	RESULT 2
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Sequence 28, Appli	; Sequence 9, Application US/09880503
Sequence 29, Appli	; Patent No. US20020131964A1
Sequence 30, Appli	GENERAL INFORMATION:
Sequence 31, Appli	APPLICANT: CINES, Douglas B
Sequence 32, Appli	APPLICANT: HIGAZI, Abd Al-Roof

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880, 503
 ; CURRENT FILING DATE: 2001-06-13
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 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
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 ; Patented No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880, 503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212, 847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 4
 ; LENGTH: 135
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-4

Query Match 99.0%; score 494; DB 10; Length 135;
 Best Local Similarity 98.8%; Pred. No. 8.4e-51; Mismatches 0; Indels 0; Gaps 0;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFRGKASTDTMGRPCLPWNNSATVLQOTYHAHRSNALQLGLGKHNHYCRNPDN 60
 Db 48 KTCYEGNGHFRGKASTDTMGRPCLPWNNSATVLQOTYHAHRSNALQLGLGKHNHYCRNPDN 60

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 Db 108 RRRPWCYVQVGLKPLVQECMVHDCAD 133

RESULT 4

US-09-984-186-12
 ; Sequence 12, Application US/09984186
 ; Patent No. US2002015101A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; APPLICANT: Fournier, Alain
 ; APPLICANT: Guittot, Jean-Dominique
 ; APPLICANT: Jung, Gerard
 ; APPLICANT: Yeh, Patrice

Query Match 99.0%; score 494; DB 10; Length 138;
 Best Local Similarity 98.8%; Pred. No. 8.6e-51; Mismatches 0; Indels 0; Gaps 0;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFRGKASTDTMGRPCLPWNNSATVLQOTYHAHRSNALQLGLGKHNHYCRNPDN 60
 Db 51 KTCYEGNGHFRGKASTDTMGRPCLPWNNSATVLQOTYHAHRSNALQLGLGKHNHYCRNPDN 110

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
 Db 111 RRRPWCYVQVGLKPLVQECMVHDCAD 136

RESULT 5

US-09-880-503-8
 ; Sequence 8, Application US/09880503
 ; Patented No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880, 503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212, 847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-503-8

Query Match 99.0%; Score 494; DB 10; Length 143;
Best Local Similarity 98.8%; Pred. No. 9e-51;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; US-09-880-503-6

RESULT 6
US-09-880-503-6
; Sequence 6, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880, 503
; CURRENT FILING DATE: 2001-06-13
; PRIORITY APPLICATION NUMBER: US 60/212, 847
; PRIORITY FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-503-6

Query Match 99.0%; Score 494; DB 10; Length 403;
Best Local Similarity 98.8%; Pred. No. 2.7e-50;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; US-09-880-503-3

RESULT 7
US-09-880-503-3
; Sequence 3, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880, 503
; CURRENT FILING DATE: 2001-06-13
; PRIORITY APPLICATION NUMBER: US 60/212, 847
; PRIORITY FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 411

Query Match 99.0%; Score 494; DB 10; Length 411;
Best Local Similarity 98.8%; Pred. No. 2.7e-50;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; US-09-880-503-3

RESULT 8
US-09-264-468B-1
; Sequence 1, Application US/09264468B
; Patent No. US20020106775A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Jiey
; APPLICANT: Nienaber, Vicki L.
; APPLICANT: Henkin, Jack
; APPLICANT: Smith, Richard A.
; APPLICANT: Walter, Karl A.
; APPLICANT: Severin, Jean M.
; APPLICANT: Edalji, Rohinton
; APPLICANT: Johnson Jr., Robert W.
; APPLICANT: Holzman, Thomas F.
; TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
; FILE REFERENCE: 6310.US.P1
; CURRENT APPLICATION NUMBER: US/09/264, 468B
; CURRENT FILING DATE: 1999-03-05
; PRIORITY APPLICATION NUMBER: US 09/036, 361
; PRIORITY FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Leader sequence
; NAME/KEY: VARIANT
; LOCATION: (279)...(279)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (302)...(302)
; OTHER INFORMATION: Xaa = any amino acid
; US-09-264-468B-1

Query Match 99.0%; Score 494; DB 10; Length 431;
Best Local Similarity 98.8%; Pred. No. 2.9e-50;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
; US-09-084-491A-3

RESULT 9
US-09-084-491A-3
; Sequence 3, Application US/09084491A
; Patent No. US20020061576A1
; GENERAL INFORMATION:

```

APPLICANT: MORE, PAUL A.
 APPLICANT: RUBEN, STEVEN M.
 APPLICANT: EBNER, REINHARD
 TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEASE
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/084,491A
 FILING DATE: 27-MAY-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOKES, ANDERS A.
 REGISTRATION NUMBER: 36,373
 REFERENCE/DOCKET NUMBER: PF378
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8504
 TELEFAX: (301) 309-8439
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein

RESULT 11
 US-09-974-298-145
 ; Sequence 145, Application US/09974298
 ; Patent No. US20020156263A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Huei-Mei
 ; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
 ; FILE REFERENCE: PA-0037 P
 ; CURRENT APPLICATION NUMBER: US/09/974,298
 ; CURRENT FILING DATE: 2001-10-04
 ; PRIORITY NUMBER: 60/238,331
 ; PRIORITY FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 194
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 145
 ; LENGTH: 562
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
 ; US-09-974-298-145

Query Match 43.3%; Score 216; DB 10; Length 372;
 Best Local Similarity 47.0%; Pred. No. 6.2e-18; Mismatches 35; Indels 0; Gaps 0;
 Matches 39; Conservative 9; Mismatches 35; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGLGKHNYCRNPDR 62
 Db 215 CYFGNGSAVRGTHSLTESGASCLPWNNSMILIGKVYTAQNPSSAQALGLGKHNYCRNPDR 274

QY 63 RPWCYVQVGLKPLVQECMVHDCA 85
 Db 275 KPWCHVLRNRLTWEYCDVPSCS 297

RESULT 10
 US-09-969-271-7
 Sequence 7, Application US/09969271
 Patent No. US20020098179A1
 GENERAL INFORMATION:
 APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
 APPLICANT: Pfizer Limited (GB and EP (GB) only);
 TITLE OF INVENTION: Pharmaceutical Combinations
 FILE REFERENCE: PCS10951APME

CURRENT APPLICATION NUMBER: US/09/969,271
 CURRENT FILING DATE: 2001-10-01
 PRIOR APPLICATION NUMBER: GB 0025473.0
 PRIOR FILING DATE: 2000-10-17
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 562
 TYPE: PRT
 ORGANISM: Homo sapiens
 S-09-969-271-7

Query Match 43.3%; Score 216; DB 10; Length 562;
 Best Local Similarity 47.0%; Pred. No. 9.7e-18; Mismatches 35; Indels 0; Gaps 0;
 Matches 39; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY Match 43.3%; Score 216; DB 10; Length 562;
 Best Local Similarity 47.0%; Pred. No. 9.7e-18; Mismatches 35; Indels 0; Gaps 0;
 Matches 39; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGLGKHNYCRNPDR 61
 Db 126 TCYEDOGISYRGTWSTAESAECTNWNSALAQPKYSGRRPDAIRLGLGNHNYCRNPDR 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCA 86
 Db 186 SKPWCYVFKAGKYSSEFCSTPACSE 210

RESULT 12
 US-09-912-559-3
 Sequence 3, Application US/09912559
 Patent No. US20020142316A1
 GENERAL INFORMATION:
 APPLICANT: ROEMISCH, JUERGEN
 APPLICANT: STOehr, HANS-ARNOLD
 APPLICANT: FEUSSNER, ANNETTE
 APPLICANT: LANG, WIEGAND
 APPLICANT: WEIMER, THOMAS
 APPLICANT: BECKER, MARGRET
 APPLICANT: NERLICH, CLAUDIA
 APPLICANT: MUTH-NAUMANN, GUDRUN
 TITLE OF INVENTION: MUTANTS OF THE FACTOR VII-ACTIVATING PROTEASE AND
 TITLE OF INVENTION: DETECTION METHODS USING SPECIFIC ANTIBODIES
 FILE REFERENCE: 06478.1457
 CURRENT APPLICATION NUMBER: US/09/912,559
 CURRENT FILING DATE: 2001-07-26
 PRIOR APPLICATION NUMBER: DE 100 36 641.4
 PRIOR FILING DATE: 2000-07-26
 PRIOR APPLICATION NUMBER: DE 100 50 040.4
 PRIOR FILING DATE: 2000-10-10
 PRIOR APPLICATION NUMBER: DE 100 52 319.6
 PRIOR FILING DATE: 2000-10-21
 PRIOR APPLICATION NUMBER: DE 101 18 706.8
 PRIOR FILING DATE: 2001-04-12

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGLGKHNYCRNPDR 62
 Db 215 CYFGNGSAVRGTHSLTESGASCLPWNNSMILIGKVYTAQNPSSAQALGLGKHNYCRNPDR 274

QY 63 RPWCYVQVGLKPLVQECMVHDCA 85
 Db 275 KPWCHVLRNRLTWEYCDVPSCS 297

Matches 39; Conservative 9; Mismatches 35; Indels 0; Gaps 0;
 Matches 39; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQLGLGKHNYCRNPDR 61
 Db 126 TCYEDOGISYRGTWSTAESAECTNWNSALAQPKYSGRRPDAIRLGLGNHNYCRNPDR 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCA 86
 Db 186 SKPWCYVFKAGKYSSEFCSTPACSE 210

OM protein - Protein search, using sw model	GenCore version 5.1.3	30	150	30.1	123	2	C61545	Plasmin (EC 3.4.21
Run on:	November 11, 2002, 12:57:46 ; Search time 38 Seconds	31	149	29.9	810	1	PLHU	plasmin (EC 3.4.21
Title:	(without alignments)	32	147.5	29.6	460	2	B61545	plasmin (EC 3.4.21
Perfect score:	217.567 Million cell updates/sec	33	147.5	29.6	810	2	I46260	plasmin (EC 3.4.21
Sequence:	PCT-US02-27855-1	34	147	29.5	937	2	A45082	neurotrophic recep
Scoring table:	BLOSUM62	35	146	29.3	810	2	B30848	plasmin (EC 3.4.21
Searched:	Gapop 10.0 , Gapext 0.5	36	143.5	28.8	711	1	A47136	macrophage-stimula
Total number of hits satisfying chosen parameters:	283224	37	143.5	28.8	943	2	B45082	neurotrophic recep
Minimum DB seq length: 0		38	142	28.5	806	2	T18840	hypothetical prote
Maximum DB seq length: 200000000		39	137	27.5	812	1	PLMS	plasmin (EC 3.4.21
Post-processing: Minimum Match 0%	Maximum Match 100%	40	134	26.9	455	2	A61545	neurotrophic recep
Listing first 45 summaries		41	134	26.9	685	1	A48289	hepatocyte growth
Database :	PIR_73:*	42	133.5	26.8	728	1	A60185	hepatocyte growth
	1: pir1:*	43	131.5	26.4	411	2	151285	macrophage-stimula
	2: pir2:*	44	131.5	26.4	716	1	A40332	hepatocyte growth
	3: pir3:*	45	131.5	26.4	728	1	JH0579	macrophage-stimula
	4: Pir4:*							hepatocyte growth
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								
SUMMARIES								
Result No.	Score	Query Match Length	DB ID	Description				ALIGNMENTS
1	494	99.0	431	1 UKHU	RESULT 1			
2	459	92.0	433	1 UKBAY	UKHU			
3	409	82.0	442	1 S18932	u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human			
4	400	80.2	432	1 JN0560	N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen			
5	383	76.8	433	1 JN0560	N; Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen			
6	381	76.4	433	1 UKMS	in form			
7	236	47.3	431	2 JS0599	C;Species: Homo sapiens (man)			
8	236	47.3	477	1 A34369	C;Date: 17-Dec-1982 #sequence_revision 04-Dec-1986 #text_change 15-Sep-2000			
9	236	47.3	477	2 JS0598	C;Accession: A00931; I52209; JF0102; A37561; I38102; S65783; A37562; A37563; A37564;			
10	226	45.3	559	1 A35029	R; Nagamine, Y.; Pearson, D.; Grattan, M.			
11	218	43.7	394	2 JS0600	Biochem. Biophys. Res. Commun. 132, 563-569, 1985			
12	216	43.3	562	1 UKHUT	A;Title: The human urokinase-plasminogen activator gene and its promoter.			
13	215	43.1	291	2 I38098	A;Reference number: A00931; MUID:85215647; PMID:2987867			
14	215	43.1	559	1 A29941	A;Accession: A00931			
15	208	41.7	477	2 JS0597	A;Molecule type: DNA			
16	204.5	41.0	558	2 JC5878	A;Cross-references: GB:X02419; PIDN:CAA26268.1; PID:91834524			
17	203.5	40.8	434	1 A35005	A;Note: the authors translated the codon ATG for residue 214 as Ile			
18	193	38.7	655	1 A46688	R; Nagai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama, Gene 36, 183-188, 1985			
19	188.5	37.8	560	1 JC4795	A;Title: Molecular cloning of cDNA coding for human preprourokinase.			
20	179.5	36.0	603	2 S28941	A;Reference number: A37561; MUID:84272706; PMID:6589620			
21	170.5	34.2	615	1 KFHU12	A;Accession: A37561			
22	158	31.7	89	2 A60140	A;Molecule type: mRNA			
23	156	31.3	120	2 E61545	A;Cross-references: GB:D00244; PIDN:9220138			
24	156	31.3	1420	2 A32869	R; Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, P.; van Els			
25	155.5	31.2	593	2 S45281	DNA 4, 139-146, 1985			
26	155	31.1	4548	1 S00657	A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human p			
27	154	30.9	812	1 PLBO	apolipoprotein(a)			
28	153	30.7	790	1 PLPG	coagulation factor			
29	152.5	30.6	169	2 A40522	apo-lipoprotein(a) (EC 3.4.21.1)			
					A;Status: preliminary			
					A;Molecule type: mRNA			
					A;Residues: 1-150, 'W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 <JAC>			
					A;Cross-references: EMBL:X02760; PIDN:935297; PID:935298			

R; Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Biochim. Biophys. Acta 1293, 83-89, 1996
 A; Title: Characterization of single chain urokinase-type plasminogen activator with a nc
 A; Reference number: S65783; MUID:96186279; PMID:8652631
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 21-140, 'L', 142-213, 'I', 215-431 <YOS>
 A; Cross-references: EMBL:DL1143; NID:91311467; PIDN:BAA01919.1; PID:9119928
 R; Gunzler, W.A.; Steffens, G.J.; Ottling, F.; Kim, S.M.A.; Frankus, E.; Flohé, L.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 1155-1165, 1982
 A; Title: The primary structure of high molecular mass urokinase from human urine.
 A; Reference number: A37562; MUID:83055084; PMID:6754569
 A; Accession: A37562
 A; Molecule type: protein
 A; Residues: 21-177 <GUN>
 R; Schäller, J.; Nick, H.; Rickli, E.E.; Gillesen, D.; Lergier, W.; Studer, R.O.
 Eur. J. Biochem. 125, 251-257, 1982
 A; Title: Human low-molecular-weight urinary urokinase. Partial characterization and prel
 A; Reference number: A37563; MUID:83003608; PMID:6749491
 A; Accession: A37563
 A; Molecule type: protein
 A; Residues: 156-176; 179-193, 'T', 195, 'T', 197-224 <SCHE>
 R; Steffens, G.J.; Gunzler, W.A.; Ottling, F.; Frankus, E.; Flohé, L.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
 A; Title: The complete amino acid sequence of low molecular mass urokinase from human uri
 A; Reference number: A37564; MUID:83055099; PMID:6754572
 A; Accession: A37564
 A; Molecule type: protein
 A; Residues: 158-410 <STE>
 R; Kentzler, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
 Biochem. Biophys. Res. Commun. 171, 401-406, 1990
 A; Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinar
 A; Reference number: A35689; MUID:90365737; PMID:2393398
 A; Accession: A35689
 A; Molecule type: protein
 A; Residues: 21-30, 'X', 32, 'X', 34-38, 'X', 40-43 <KEN>
 A; Note: identification of a fucose and attempt to determine its attachment site
 R; Rabbani, S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazar, A.; Henkin, J.; Goltz
 Biochem. Biophys. Res. Commun. 173, 1058-1064, 1990
 A; Title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li
 A; Reference number: A36697; MUID:91097529; PMID:2125213
 A; Accession: A36697
 A; Molecule type: protein
 A; Residues: 21-34 <RAB>
 R; Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
 Submitted to the Brookhaven Protein Data Bank, July 1993
 A; Reference number: A51255; PDB:1KDU
 A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 R; Li, X.; Smith, R.A.G.; Dobson, C.M.
 Biochemistry 31, 9562-9571, 1992
 A; Title: Sequential (1)H-NMR assignments and secondary structure of the kringle domain f
 A; Reference number: A44375; MUID:93003110; PMID:1327118
 A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
 R; Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettlesheim, D.G.; Mazar, A.P.; Olejniczak,
 submitted to the Brookhaven Protein Data Bank, January 1994
 A; Reference number: A66822; PDB:1URK
 A; Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
 R; Spraggan, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.;
 submitted to the Brookhaven Protein Data Bank, July 1995
 A; Reference number: A66058; PDB:1LMW
 A; Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 163-175; 179-426
 C; Comment: this enzyme is found in urine in a high molecular mass form, consisting of a
 C; Comment: urokinase-type plasminogen activator proteolytically activates plasminogen, a
 C; Genetcs:
 A; Gene: GDB:PLAU
 A; Cross-references: GDB:119497; OMIM:191840
 A; Map position: 10q24-10q24
 A; Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
 C; Function:
 A; Description: proteolytically activates plasminogen
 A; Pathway: fibrinolysis
 C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try

RESULT 2
 UKBAY
 u-Plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
 C; Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
 C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
 C; Accession: S14687; S08651
 R; Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
 Nucleic Acids Res. 18, 3411, 1990
 A; Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasmin
 A; Reference number: S14687; MUID:90287734; PMID:2113276
 A; Accession: S14687
 A; Molecule type: mRNA
 A; Residues: 1-433 <AUY>
 A; Cross-references: EMBL:X51935; NID:938130; PIDN:CNA36200.1; PID:938131
 C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology;
 C; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
 F; 1-20/Domain: signal sequence #status predicted <SIG>
 F; 21-176/Product: plasminogen activator chain A #status predicted <ACH>
 F; 30-61/Domain: EGF homology <EGF>
 F; 69-150/Domain: kringle homology <KRG>
 F; 178-433/Product: plasminogen activator chain B #status predicted <BCB>
 F; 178-421/Domain: trypsin homology <TRY>
 F; 167-298, 208-224, 216-287, 315-384, 347-363, 374-402/disulfide bonds: #status predicted
 F; 223, 274, 378/Active site: His, Asp, Ser #status predicted
 F; 324/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match Best Local Similarity 92.0%; Score 459; DB 1; Length 433;
 Matches 80; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Result 3
 UKB
 u-Plasminogen activator (EC 3.4.21.73) precursor - pig
 N; Alternative names: uPA
 C; Species: Sus scrofa domestica (domestic Pig)
 C; Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998

C;Accession: A00932
 R;Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984
 A;Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
 A;Reference number: A00932; MUID:85087954; PMID:6096832
 A;Accession: A00932
 A;Molecule type: DNA
 A;Residues: 1-240, 'H', 242-442 <NAGL>
 A;Experimental source: kidney cell line LLC-PK1
 R;Nagamine, Y.
 Submitted to the Protein Sequence Database, December 1986
 A;Reference number: A37566
 A;Contents: annotation; correction to residue 241
 C;Genetics:
 A;Introns: 19/3; 31/1; 67/1; 125/2; 165/1; 238/2; 288/1; 335/1; 384/3
 C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
 C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-188/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
 F;33-64/Domain: EGF homology <EGF>
 F;72-153/Domain: kringle homology <KRG>
 F;190-442/Product: urokinase-type plasminogen activator chain B #status predicted <BCB>
 F;152/Binding site: trypsin homology <TRY>
 F;179-310, 220-236, 228-299, 324-393, 356-372, 383-411/Disulfide bonds: #status predicted
 F;235, 286, 387/Active site: His, ASP, Ser #status predicted

Query Match 82.0%; Score 409; DB 1; Length 442;
 Best Local Similarity 82.4%; Pred. No. 1.1e-37;
 Matches 70; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60
 Db 70 QTCFEEGNGHHSYRGKANTNTGGRPCLPWNNSATVLLNTYHAHRPDALQQLGLGKHNHYCRNPDN 129

QY 61 RRRPWCYVQVGLKPLVQECMVHDCA 85
 Db 130 QRRPWCVYQVGLKQFVQECMVQDCS 154

RESULT 4
 S18932
 u-plasminogen activator (EC 3.4.21.73) precursor - rat
 N;Alternate names: plasminogen activator, urokinase-type; urinary plasminogen activator
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 18-Oct-1989 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
 C;Accession: S24604; I60186; S18932
 R;Rabbani, S.A.
 submitted to the EMBL Data Library, April 1992
 A;Reference number: S24604
 A;Accession: S24604
 A;Molecule type: mRNA
 A;Residues: 1-15, 'H', 17-23, 'G', 25-331, 'N', 333-432 <RAB>
 A;Cross-references: EMBL:X65651; NID:957456; PIDN:CAA46601.1; PID:957457

Query Match 82.0%; Score 409; DB 1; Length 442;
 Best Local Similarity 82.4%; Pred. No. 1.1e-37;
 Matches 70; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60
 Db 70 QTCFEEGNGHHSYRGKANTNTGGRPCLPWNNSATVLLNTYHAHRPDALQQLGLGKHNHYCRNPDN 129

Query Match 80.2%; Score 400; DB 1; Length 432;
 Best Local Similarity 80.0%; Pred. No. 1.1e-36;
 Matches 68; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60
 Db 68 KTCYHNGNGOSYRGKANTDTKGRPCLAWNNSPAVLQQTNAHRSDALSLGLGKHNHYCRNPDN 129

QY 61 RRRPWCYVQVGLKPLVQECMVHDCA 85
 Db 128 QRRPWCVYQVGLKQFVQECMVQDCS 152

RESULT 5
 JN0560
 u-Plasminogen activator (EC 3.4.21.73) precursor - bovine
 N;Alternate names: uPA
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C;Accession: JN0560
 R;Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
 Gene 125, 177-183, 1993
 A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and in
 A;Reference number: JN0560; MUID:93216119; PMID:8385052
 A;Accession: JN0560
 A;Molecule type: mRNA
 A;Residues: 1-433 <KRA>
 A;Cross-references: GB:L03546; NID:9163800; PIDN:AA51419.1; PID:9163801

Query Match 80.2%; Score 400; DB 1; Length 432;
 Best Local Similarity 80.0%; Pred. No. 1.1e-36;
 Matches 68; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60
 Db 70 QTCFEEGNGHHSYRGKANTNTGGRPCLPWNNSATVLLNTYHAHRPDALQQLGLGKHNHYCRNPDN 129

Query Match 76.8%; Score 383; DB 1; Length 433;
 Best Local Similarity 75.3%; Pred. No. 8.4e-35;
 Matches 64; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQQLGLGKHNHYCRNPDN 60
 Db 70 QTCFEEGNGHHSYRGKANTNTGGRPCLPWNNSATVLLNTYHAHRPDALQQLGLGKHNHYCRNPDN 129

RESULT 6
 UKMS
 u-plasminogen activator (EC 3.4.21.73) precursor - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
 C;Accession: A29420; A24615

R; Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
 Biochemistry 26, 8270-8279, 1987
 A; Title: The murine urokinase-type plasminogen activator gene.
 A; Reference number: A29420; MUID:88163489; PMID:2831940
 A; Molecule type: DNA
 A; Residues: 1-433 <DEG>
 A; Cross-references: GB:J17922; NID:9202296; PIDN:AAA40539.1; PID:9202297
 R; Belin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Eur. J. Biochem. 148, 225-232, 1985
 A; Title: Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase
 A; Reference number: A24615; MUID:85179474; PMID:2985383
 A; Accession: A24615
 A; Molecule type: mRNA
 A; Residues: 1-433 <BEL>
 A; Cross-references: GB:X02389; NID:955127; PIDN:CAA26231.1; PID:955128
 C; Genetics:
 A; Introns: 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3
 C; Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
 C; Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine protease
 F; 1-20/Domain: signal sequence #status predicted <SIG>
 F; 21-178/Domain: urokinase-type plasminogen activator chain A #status predicted <ACH>
 F; 32-63/Domain: EGF homology <EGF>
 F; 71-152/Domain: kringle homology <KRG>
 F; 180-433/Domain: urokinase-type plasminogen activator chain B #status predicted <BCH>
 F; 169-301, 211-227, 219-290, 315-384, 347-363, 374-402/Disulfide bonds: #status predicted
 F; 226, 277, 378/Active site: His, Asp, Ser #status predicted
 Query Match 76.4%; Score 381; DB 1; Length 433;
 Best Local Similarity 72.9%; Pred. No. 1.4e-34;
 Matches 62; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNHYCRNPDN 60
 Db 69 KTCYHNGDSDYRGKANTDTKGRPCLAWNAPAVLQKPNYNAHRPDAISLGLGKHNHYCRNPDN 128
 QY * 61 RRPWPCYVQVGLKPLVQECMVHDCA 85
 Db 129 QKRPWPCYVQIGLROFVQECMVHDCA 153
 RESULT 7
 JS0599
 t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
 N; Alternative names: tissue plasminogen activator
 C; Species: Desmodus rotundus (common vampire bat)
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C; Accession: JS0599
 R; Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
 Gene 105, 229-237, 1991
 A; Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A; Reference number: JS0597; MUID:92039036; PMID:1937019
 A; Accession: JS0599
 A; Molecule type: mRNA
 A; Residues: 1-431 <KRA>
 A; Cross-references: GB:M63989; NID:9166076; PIDN:AAA31594.1; PID:9166077
 C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 F; 1-21/Domain: signal sequence #status predicted <SIG>
 F; 22-36/Domain: propeptide #status predicted <PRO>
 F; 37-431/Product: plasminogen activator beta #status predicted <PLA>
 F; 41-74/Domain: EGF homology <EGF>
 F; 82-163/Domain: kringle homology <KRG>
 F; 180-425/Domain: trypsin homology <TRY>
 F; 41-52, 46-63, 65-74, 82-163, 103-145, 134-158, 168-299, 211-227, 219-288, 313-388/Disulfide bond
 F; 139-352/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 179-180/Cleavage site: His-Ser (plasmin) #status predicted
 F; 226-275, 382/Active site: His, Asp, Ser #status predicted
 F; 345-361, 378-406/Disulfide bonds: #status predicted
 Query Match 47.3%; Score 236; DB 2; Length 431;
 Best Local Similarity 48.8%; Pred. No. 1.7e-18;

RESULT 8
 A34369
 t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
 C; Species: Megaderma lyra
 C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C; Accession: A34369
 R; Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Ja
 J. Biol. Chem. 264, 17947-17952, 1989
 A; Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plas
 A; Reference number: A34369; MUID:90036867; PMID:2509450
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-477 <GAR>
 A; Cross-references: GB:J05082; NID:9166080; PIDN:AAA31596.1; PID:9166081
 C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C; Keywords: fibronlysis; glycoprotein; hydrolase; kringle; serine protease
 F; 1-21/Domain: signal sequence #status predicted <SIG>
 F; 22-36/Domain: propeptide #status predicted <PRO>
 F; 37-477/Domain: plasminogen activator #status predicted <PLA>
 F; 42-79/Domain: fibronectin type I repeat homology <IFIA>
 F; 87-120/Domain: EGF homology <EGF>
 F; 128-209/Domain: kringle homology <KRG>
 F; 226-471/Domain: propeptide #status predicted <PRO>
 F; 42-72, 70-79, 87-98, 92-109, 111-200, 128-209, 149-191, 180-204, 214-345, 257-273, 265-334, 35
 F; 272, 321, 428/Active site: His, Asp, Ser #status predicted
 Query Match 47.3%; Score 236; DB 1; Length 477;
 Best Local Similarity 48.8%; Pred. No. 1.9e-18;
 Matches 41; Conservative 13; Mismatches 30; Indels 0; Gaps 0;
 QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNHYCRNPDN 61
 Db 81 TCYKDGVTYRGTWSTSESGAQCINWNNSNLTRRTYNGRRSDAITLGLGHNHYCRNPDN 140
 QY 62 RRPWPCYVQVGLKPLVQECMVHDCA 85
 Db 141 SKPWCYVVIKASKFILEFCCSVPC 164
 RESULT 9
 JS0598
 t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
 N; Alternative names: tissue plasminogen activator
 C; Species: Desmodus rotundus (common vampire bat)
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C; Accession: JS0598
 R; Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
 Gene 105, 229-237, 1991
 A; Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A; Reference number: JS0597; MUID:92039036; PMID:1937019
 A; Accession: JS0598
 A; Molecule type: mRNA
 A; Residues: 1-477 <KRA>
 A; Cross-references: GB:M63988; NID:9166074; PIDN:AAA31593.1; PID:9166075
 C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 F; 1-21/Domain: signal sequence #status predicted <SIG>
 F; 22-36/Domain: propeptide #status predicted <PRO>
 F; 37-477/Domain: plasminogen activator alpha-2 #status predicted <PLA>
 F; 42-79/Domain: fibronectin type I repeat homology <IFIA>
 F; 87-120/Domain: EGF homology <EGF>

Query Match 47.3%; Score 236; DB 2; Length 477;
 Best Local Similarity 48.8%; Pred. No. 1.9e-18;
 Matches 41; Conservative 13; Mismatches 30; Indels 0; Gaps 0;

Qy 2 TCYEGNGHRYRGKASTDTMGRPCLPWNSATVLOQTYHAHRNSNALQLGKHNHCNRPDNR 61
 |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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RESULT 11
 JS0600 t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
 N;Alternate names: tissue plasminogen activator
 C;Species: Desmodus rotundus (common vampire bat)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C;Accession: JS0600
 R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Gene 105, 229-237, 1991
 A;Title: The plasminogen activator family from the salivary gland of the vampire bat
 A;Reference number: JS0597; MUID:92039036; PMID:1937019
 A;Accession: JS0600
 A;Molecule type: mRNA
 A;Cross-references: GB: M63990; NID:9166078; PIDN:AAA31595.1; PID:9166079
 A;Note: the authors translated the codon ATC for residue 75 as Thr
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F;1-21/Domain: signal sequence #status predicted
 F;22-36/Domain: propeptide #status predicted <PRO>
 F;37-394/Product: plasminogen activator gamma #status predicted <PLA>
 F;45-126/Domain: trypsin homology <KRG>
 F;143-388/Domain: trypsin homology <TRY>
 F;45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bond
 F;142-143/Cleavage site: His-ser (plasmin) #status predicted
 F;189,238,345/Active site: His, Asp, Ser #status predicted
 F;315/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 43.7%; Score 218; DB 2; Length 394;
 Best Local Similarity 45.2%; Pred. No. 1.6e-16;
 Matches 38; Conservative 12; Mismatches 34; Indels 0; Gaps 0;

Qy 2 TCYEGNGHRYRGKASTDTMGRPCLPWNSATVLOQTYHAHRNSNALQLGKHNHCNRPDNR 61
 |||:||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 44 TCYKDQGVTYRGTWSTSESGAQCINWNNSNLIRRNGRMPEAVKLGKHNHCNRPDGA 103
 R;NY, T.; Leonardsson, G.; Hsueh, A.J.W.
 DNA 7, 671-677, 1988
 A;Title: Cloning and characterization of a cDNA for rat tissue-type Plasminogen activator
 A;Reference number: A31597; MUID:89170114; PMID:3148445
 A;Accession: A31597
 A;Molecule type: mRNA
 A;Residues: 1-379, 'K', 381-559 <NYT>
 A;Cross-references: GB: M23697; NID:9530159; PIDN:AAA41812.1; PID:9530160
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-29/Domain: propeptide #status predicted <PRO>
 F;30-59/Product: t-plasminogen activator #status predicted <MAT>
 F;30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
 F;38-75/Domain: fibronectin type I repeat homology <1FL1>
 F;83-116/Domain: EGF homology <EGF>
 F;213-294/Domain: kringle homology <KR2>
 F;309-559/Product: t-plasminogen activator chain B #status predicted <BCB>
 F;309-553/Domain: trypsin homology <TRY>
 F;149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;308-309/Cleavage site: carbohydrate (Asn) (covalent) #status predicted
 F;

A; Experimental source: embryonic lung fibroblast IMR-90 cells
 A; Note: part of this sequence, including the amino end of the mature protein, was confirmed by peptide sequencing
 R; Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett, N.; Nature 301, 214-221, 1983
 A; Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Escherichia coli
 A; Reference number: A93293; MUID:83115262; PMID:6337343
 A; Accession: A93293
 A; Molecule type: mRNA
 A; Residues: 1-562 <PEN>
 A; Cross-references: GB:L00141
 A; Experimental source: melanoma cells
 R; Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.; Nucleic Acids Res. 16, 5695, 1988
 A; Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fibroblasts
 A; Reference number: S02125; MUID:88262579; PMID:3133640
 A; Accession: S02125
 A; Status: translation not shown
 A; Molecule type: mRNA
 A; Residues: 1-562 <SAS>
 A; Cross-references: EMBL:X07393; NID:g37243; PIDN:CAA30302.1; PID:g37244
 A; Experimental source: fetal lung cells
 R; Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Matsunaga, T.; FEBS Lett. 189, 145-149, 1985
 A; Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen activator
 A; Reference number: A91343; MUID:85285620; PMID:3896853
 A; Accession: A91343
 A; Molecule type: mRNA
 A; Residues: 1-38, 'G', 86-433, 'E', 435-562 <KAG>
 A; Experimental source: Detroit 562 cells; ATCC 138
 R; Edlund, T.; NY, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.; Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
 A; Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activator
 A; Reference number: A93951; MUID:83169656; PMID:6572897
 A; Accession: A93951
 A; Molecule type: mRNA
 A; Residues: 251-358 <EDL>
 A; Experimental source: melanoma cells
 R; Pohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.; Biochemistry 23, 3701-3707, 1984
 A; Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived amino acid sequence.
 A; Reference number: A90488; MUID:85000468; PMID:6433976
 A; Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and R; Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.; FEBS Lett. 168, 29-32, 1984
 A; Title: Differences between uterine and melanoma forms of tissue plasminogen activator.
 A; Reference number: A91322; MUID:84158956; PMID:6538514
 A; Accession: A91322
 A; Molecule type: protein
 A; Residues: 33-45;311-320 <POH>
 A; Experimental source: uterus
 A; Note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
 R; van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.; J. Biol. Chem. 261, 14214-14218, 1986
 A; Reference number: A37567; MUID:87033611; PMID:3021732
 A; Contents: annotation; fibrin binding site
 R; Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Engelman, B.; EMBO J. 5, 3525-3530, 1986
 A; Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen activator.
 A; Reference number: A37568; MUID:87161761; PMID:3030730
 A; Contents: annotation; fibrin binding site
 R; Dodd, I.; Nunn, B.; Robinson, J.H.; Thromb. Haemost. 59, 523-528, 1988
 A; Title: Isolation, identification and pharmacokinetic properties of human tissue-type plasminogen activator
 A; Reference number: A60902; MUID:89044681; PMID:3142086
 A; Contents: annotation; novel forms of expressed recombinant t-PA
 R; Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Entage, J.S.; Opdenakker, G.; Mol. Biol. Med. 3, 279-292, 1986
 A; Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expression
 A; Reference number: A54645; MUID:86284200; PMID:3090401
 A; Accession: A54645
 A; Molecule type: mRNA
 A; Residues: 1-562 <HAR>

A; Cross-references: GB:MI15518; NID:g190031; PIDN:AAA6011.1; PID:g190032
 A; Note: parts of this sequence were confirmed by peptide sequencing
 R; Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.; DNA 6, 461-472, 1987
 A; Title: Expression of human uterine tissue-type plasminogen activator in mouse cells
 A; Reference number: I60110; MUID:88054470; PMID:2824147
 A; Accession: I60110
 A; Molecule type: mRNA
 A; Status: translated from GB/EMBL/DDBJ
 A; Residues: 1-562 <RES>
 A; Molecule type: mRNA
 A; Status: translated from GB/EMBL/DDBJ
 A; Residues: 1-562 <RES>
 A; Molecule type: mRNA
 A; Status: translated from GB/EMBL/DDBJ
 A; Residues: 1-36 <RE2>
 A; Cross-references: GB:MI1890; NID:g339837; PIDN:AAA61213.1; PID:g339839
 C; Comment: Cleavage by plasmin or trypsin produces two chains held together by a single Arg-Val bond.
 C; Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond.
 C; Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
 C; Genetics:
 A; Gene: GDB:PLAT
 A; Cross-references: GDB:119496; OMIM:173370
 A; Map position: 8p12-8p12
 A; Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3;
 C; Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat;
 C; Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase F; 1-23/Domain: propeptide #status predicted <SIG>
 F; 24-32/Domain: propeptide #status predicted <PRO>
 F; 33-562/Product: t-plasminogen activator #status experimental <MAT>
 F; 33-310/Product: t-plasminogen activator chain A #status experimental
 F; 41-78/Domain: fibronectin type I repeat homology <IF1>
 F; 86-119/Domain: EGF homology <EGE>
 F; 127-208/Domain: kringle homology <KR1>
 F; 215-296/Domain: kringle homology <KR2>
 F; 311-562/Product: t-plasminogen activator chain B #status experimental <BCB>
 F; 311-556/Domain: trypsin homology <TRY>
 F; 41-71,69-78,86-97,91-108,119-127,208,148-190,179-203,215-296,236-278,267-291,29
 F; 152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F; 219/Binding site: carbohydrate (Asn) (covalent) (Partial) #status experimental
 F; 310-311/Cleavage site: Arg-Tle (plasmin, trypsin) #status experimental
 F; 357,406/Active site: His, Asp #status predicted
 F; 513/Active site: Ser #status experimental

Query Match 43.3%; Score 216; DB 1; Length 562;
 Best Local Similarity 47.0%; Pred. No. 3.7e-16;
 Matches 39; Conservative 9; Mismatches 35; Indels 0; Gaps 0;

QY	3	CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLOQTYHAHRSNALQGLGKHNHCNRPDNR	62
Db	215	CYFGNGSAYRGTHSILTESGASCLPWNNSMILIGKVTAQNPSAQALGLGKHNHCNRPDGA	274

QY 63 RPWCYVQVGLKPLVQECMVHDCA 85
 Db 275 KPWCHVLRNRLTWYCDVPSCS 297

RESULT 13
 138098 t-plasminogen activator precursor, inactive endothelial splice form - human
 N; Alternate names: tissue plasminogen activator
 C; Species: Homo sapiens (man)
 C; Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
 C; Accession: I38098; S01678
 R; Siebert, P.D.; Fong, K.
 Nucleic Acids Res 18, 1086, 1990
 A; Title: Variant tissue type plasminogen activator (PLAT) cDNA obtained from human embryo
 A; Reference number: I38098; MUID:90192128; PMID:1969145
 A; Accession: I38098
 A; Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA
 A;Residues: 1-291 <SIE>
 A;Cross-references: EMBL:XL3097; NID:g35282; PIDN:CAA31489.1; PID:g35283
 C;Comment: For the main splice form, see PIR:UKHUT. This form probably does not have prc
 C;Genetics:
 A;Gene: GDB:PLAT
 A;Cross-references: GDB:119496; OMIM:173370
 A;Map position: 8p12-8p12
 A;Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C;Keywords: alternative splicing; fibrinolysis; glycoprotein; kringle
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-32/Domain: propeptide #status predicted <PRO>
 F;33-291/Product: t-plasminogen activator, inactive endothelial splice form #status pred
 F;41-78/Domain: fibronectin type I repeat homology <1FA>
 F;86-119/Domain: EGF homology <EGF>
 F;127-208/Domain: kringle homology <KR1>
 F;215-291/Domain: kringle homology #status atypical <KR2>
 F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203/disulfide bonds: #status pred
 F;41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203/disulfide bonds: #status pred
 Query Match 43.1%; Score 215; DB 2; Length 291;
 Best Local Similarity 45.9%; Pred. No. 2.5e-16;
 Matches 39; Conservative 9; Mismatches 37; Indels 0; Gaps 0;
 Qy 2 TCYEGNGHFEYRGKASTDTMGRPCLPWNNSATVLOQTYAHRSNALQIGLGHKHNCRNPDRN 61
 Db 126 TCYEDQGQISYRGTWSTAESGAECINWNSSVLSKPYNARRPNNAIKLGLGNHNYCRNPDRD 185
 Qy 62 RRPWCYVQVGLKPLVQECMVHDC 84
 Db 183 LKPWCYVFKAGKYTTEFCSTPAC 205

RESULT 15
 JS0597
 t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat
 N;Alternate names: tissue plasminogen activator
 C;Species: Desmodus rotundus (common vampire bat)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C;Accession: JS0597
 R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boldol, W.; Bringmann, P.; Alagon, A.;
 Gene 105, 229-237, 1991
 A;Title: The plasminogen activator family from the salivary gland of the vampire bat
 A;Reference number: JS0597; MUID:92039036; PMID:1937019
 A;Accession: JS0597
 A;Molecule type: mRNA
 A;Residues: 1-477 <KRA>
 A;Cross-references: GB:63987; NID:g166070; PIDN:AAA31591.1; PID:g166071
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-36/Domain: propeptide #status predicted <PRO>
 C;Accession: A29941; S48205; S48207; S48206
 R;Rickles, R.J.; Darrow, A.L.; Strickland, S.
 J. Biol. Chem. 263, 1563-1569, 1988
 A;Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator mRNA
 A;Reference number: A29941; MUID:88087303; PMID:2826484
 A;Accession: A29941
 A;Molecule type: mRNA
 A;Residues: 1-559 <RIC>
 A;Cross-references: GB:J03520; NID:g202109; PIDN:AAA40470.1; PID:g202110
 R;LiJnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A;Title: Characterization of the murine plasma fibrinolytic system.
 A;Reference number: S48202; MUID:95010076; PMID:7523120
 A;Accession: S48205
 A;Molecule type: protein
 A;Residues: 33-37, 'X', 39-40 <LIJ>
 A;Accession: S48207
 A;Molecule type: protein
 A;Residues: 309-316 <LI2>
 A;Accession: S48206
 A;Molecule type: protein
 A;Residues: 33-37, 'X', 39-40 <LIW>
 C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F;1-17/Domain: signal sequence #status predicted <SIG>
 F;18-29/Domain: propeptide #status predicted <PRO>
 F;30-559/Product: t-plasminogen activator #status predicted <MAT>
 F;30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
 F;38-75/Domain: fibronectin type I repeat homology <1FL>
 F;83-116/Domain: EGF homology <EGF>
 F;124-205/Domain: kringle homology <KR1>
 F;213-294/Domain: kringle homology <KR2>
 F;309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
 F;309-553/Domain: trypsin homology <TRY>
 F;38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-4

Search completed: November 11, 2002, 13:02:46
 Job time: 39 secs

Copyright (c) 1993 - 2002 Compugen Ltd.	GenCore version 5.1.3				
Run on:	November 11, 2002, 11:40:46 ; Search time 21 Seconds				
	(without alignments)				
	169.855 Million cell updates/sec				
Title:	PCT-US02-27855-1				
Perfect score:	499				
Sequence:	1 KTCVEGNNGHFRGKASTDTM..... YVQVGLKPLVQECMVHDCAD 86				
Scoring table:	BLOSUM62				
	Gapop 10.0 , Gapext 0.5				
Searched:	112892 seqs, 41476328 residues				
Total number of hits satisfying chosen parameters:	112892				
Minimum DB seq length:	0				
Maximum DB seq length:	200000000				
Post-processing:	Minimum Match 0%				
	Maximum Match 100%				
	Listing first 45 summaries				
Database :	Swissprot_40:*				
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	8				
SUMMARIES					
Result No.	Score	Query	Match Length	DB ID	Description
1	494	99.0	431	1 UROK_HUMAN	P00749 homo sapien
2	459	92.0	433	1 UROK_PAPCY	P16227 papio cynoc
3	409	82.0	442	1 UROK_PIG	P04185 sus scrofa
4	400	80.2	432	1 UROK_RAT	P29598 rattus norv
5	383	76.8	433	1 UROK_BOVIN	Q05589 bos taurus
6	381	76.4	433	1 UROK_MOUSE	P06869 mus musculus
7	236	47.3	431	1 URTB_DESRO	P98121 desmodus ro
8	236	47.3	477	1 URT2_DESRO	P15638 desmodus ro
9	226	45.3	559	1 TPA_RAT	P19637 rattus norv
10	218	43.7	394	1 URTG_DESRO	P49150 desmodus ro
11	216	43.3	562	1 TPA_HUMAN	P00750 homo sapien
12	215	43.1	559	1 TPA_MOUSE	P12114 mus musculus
13	214	42.9	566	1 TPA_BOVIN	Q28198 bos taurus
14	208	41.7	477	1 URT1_DESRO	P98119 desmodus ro
15	203.5	40.8	434	1 UROK_CHICK	P15120 gallus gallus
16	193	38.7	655	1 HGFA_HUMAN	Q04756 homo sapien
17	188	37.7	653	1 HGFA_MOUSE	Q9r098 mus musculus
18	179.5	36.0	603	1 FA12_CAVPO	Q04962 cavia porc
19	170.5	34.2	615	1 FA12_HUMAN	P00748 homo sapien
20	158	31.7	473	1 KREM_MOUSE	Q99n43 mus musculus
21	158	31.7	473	1 KREM_RAT	Q924s4 rattus norv
22	156	31.3	1420	1 APOA_MACMU	P14417 macaca mulatta
23	155.5	31.2	593	1 FA12_BOVIN	P98140 bos taurus
24	155	31.1	475	1 KREM_HUMAN	Q96mb8 homo sapien
25	155	31.1	4548	1 APOA_HUMAN	P08519 homo sapien
26	154	30.9	812	1 PLMN_BOVIN	P06868 bos taurus
27	153	30.7	790	1 PLMN_PIG	P06867 sus scrofa
28	152.5	30.6	169	1 PLMN_RAT	Q01177 rattus norv
29	149	29.9	810	1 PLMN_HUMAN	P00747 homo sapien
30	148.5	29.8	944	1 ROR2_MOUSE	Q9z138 mus musculus
31	147.5	29.6	810	1 PLMN_ERIEU	Q29485 erinaceus e
32	147	29.5	937	1 ROR1_HUMAN	Q01973 homo sapien
33	147	29.5	937	1 ROR1_MOUSE	Q9z139 mus musculus

34	146	29.3	810	1 PLMN_MACMU
35	143.5	28.8	711	1 HGFL_HUMAN
36	143.5	28.8	943	1 ROR2_HUMAN
37	143	28.7	333	1 PLMN_CANFA
38	137	27.5	812	1 PLMN_MOUSE
39	133.5	26.8	728	1 HGFL_MOUSE
40	131.5	26.4	716	1 HGFL_MOUSE
41	131.5	26.4	728	1 HGF_HUMAN
42	131.5	26.4	728	1 HGF_RAT
43	126	25.3	325	1 PLMN_PETMA
44	125	25.1	622	1 THR2_HUMAN
45	124.5	24.9	618	1 THR2_MOUSE

P12545	macaca mulatta
P26927	homo sapien
Q01974	homo sapien
P80009	canis familiaris
P20918	mus musculus
Q08048	mus musculus
P14210	mus musculus
P17945	rattus norvegicus
P33574	petromyzon marinus
P0734	homo sapiens
P19221	mus musculus

ALIGNMENTS

RT "Identification and primary sequence of an unspliced human urokinase
 RT POLY(A)+ RNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4727-4731(1984).
 RN [8]
 RP SEQUENCE OF 21-177.
 RX Gunzler W.A.; Pubmed=6754569;
 RA Flohe L.;
 RT "the primary structure of high molecular mass urokinase from human
 urine. The complete amino acid sequence of the A chain.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
 RN [9]
 RP SEQUENCE OF 156-176 AND 179-224;
 RX MEDLINE=83003608; PubMed=6749491;
 RA Schaller J.; Nick H.; Rickle E.E.; Gillessen D.; Lergier W.,
 Studer R.O.;
 RT "Human low-molecular-weight urinary urokinase. Partial
 characterization and preliminary sequence data of the two polypeptide
 chains.";
 RL Eur. J. Biochem. 125:251-257(1982).
 RN [10]
 RP SEQUENCE OF 158-410.
 RX MEDLINE=8305509; PubMed=6754572;
 RA Steffens G.J.; Gunzler W.A.; Ottung F.; Frankus E.; Flohe L.;
 RT "The complete amino acid sequence of low molecular mass urokinase
 from human urine.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=96000858; PubMed=8591045;
 RA Spraggon G.; Phillips C.; Dobson C.M.; Stuart D.T.; Jones E.Y.;
 RA "The crystal structure of the catalytic domain of human
 urokinase-type plasminogen activator.";
 RT Structure 3:681-691(1995).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
 RX MEDLINE=20266327; PubMed=1080574;
 RA Sperl S.; Jacob U.; Arroyo de Prada N.; Sturzebecher J.; Wilhelm O.G.,
 RA "Bode W.; Magdolen V.; Huber R.; Moroder L.;
 RA "(4-aminomethyl)phenylguanidine derivatives as nonpeptidic highly
 selective inhibitors of human urokinase";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118(2000).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=89127526; PubMed=2536903;
 RA Oswald R.E.; Bogusky M.J.; Bamberger M.; Smith R.A.G.; Dobson C.M.;
 RT "Dynamics of the multidomain fibrinolytic protein urokinase from two-
 dimensional NMR";
 RL Nature 337:579-582(1989).
 RN [14]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=93003110; PubMed=1327118;
 RA Li X.; Smith R.A.G.; Dobson C.M.;
 RT "sequential 1H NMR assignments and secondary structure of the kringle
 domain from urokinase";
 RL Biochemistry 31:9562-9571(1992).
 RN [15]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=94149701; PubMed=8107091;
 RA Li X.; Bokman A.M.; Llinas M.; Smith R.A.G.; Dobson C.M.;
 RT "solution structure of the kringle domain from urokinase-type
 plasminogen activator";
 RL J. Mol. Biol. 235:1548-1559(1994).
 RP VARIANT LEU-141.
 RX MEDLINE=96186279; PubMed=8652631;
 RA Yoshimoto M.; Ushiyama Y.; Sakai M.; Tamaki S.; Hara H.; Takahashi K.,
 RA Sawasaki Y.; Hanada K.;
 RT "Characterization of single chain urokinase-type plasminogen
 activator with a novel amino-acid substitution in the kringle
 structure";
 RL Biochim. Biophys. Acta 1293:83-89(1996).
 RN [17]
 RP VARIANT LEU-141.
 RX MEDLINE=97218551; PubMed=9065988;
 RA Conne B.; Berczy M.; Belin D.;
 RT "Detection of polymorphisms in the human urokinase-type plasminogen
 activator gene.";
 RL Thromb. Haemost. 77:434-435(1997).
 RN [18]
 RP ERRATUM.
 RA Conne B.; Berczy M.; Belin D.;
 RL Thromb. Haemost. 78:973-973(1997).
 RN [19]
 RP VARIANT LEU-141.
 RX MEDLINE=97337920; PubMed=9194591;
 RA Turkmen B.; Schmitt M.; Schmalfeldt B.; Trommler P.; Hell W.,
 Cretzburg S.; Graeff H.; Magdolen V.;
 RT "Mutational analysis of the genes encoding urokinase-type plasminogen
 activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer.";
 RT Electrophoresis 18:686-689(1997).
 CC -1- FUNCTION: POTENT PLASMINOGEN ACTIVATOR AND IS CLINICALLY USED FOR
 CC THERAPY OF THROMBOLYTIC DISORDERS.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-1-val bond in
 CC plasminogen to form plasmin.
 CC -1- SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS
 CC OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A
 CC LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 155 IN THE LOW
 CC MOLECULAR MASS FORM TO YIELD A SHORT A1 CHAIN.
 CC -1- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used
 CC in Pulmonary Embolism (PE) to initiates fibrinolysis.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY SI.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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 or send an email to license@isb-sib.ch).
 CC
 EMBL; X02419; CAA26268.1;
 DR EMBL; M15476; AAA61253.1; -.
 DR EMBL; D00244; BAA00175.1; -.
 DR EMBL; D11143; BAA01919.1; -.
 DR EMBL; X02760; CAA26535.1; -.
 DR EMBL; AF377330; AAK53822.1; -.
 DR EMBL; BC013575; AAH13575.1; -.
 DR EMBL; K03226; AAC97138.1; -.
 DR EMBL; K02286; AAA61252.1; -.
 DR EMBL; A21571; CAA01559.1; -.
 DR EMBL; A18397; CAA01390.1; -.
 DR PIR; A00931; UKHU.
 DR PIR; A32974; A32974.
 DR PDB; 1KDU; 31-OCT-93.
 DR PDB; 1LMW; 29-JAN-96.
 DR PDB; 1URK; 08-MAY-95.
 DR PDB; 1EJN; 17-MAY-00.
 DR MEROPS; S01.231.
 DR GLYCOSUITEDB; P00749; -.
 DR Genew; HGNC:9052; PLAU.
 DR MIM: 191840; -.
 DR Interpro; IPR001314; Chymotrypsin.
 DR Interpro; IPR000561; EGF-like.
 DR Interpro; IPR000001; Kringle.
 DR Interpro; IPR001254; Ser_protease_TRY.
 DR Pfam; PF00051; kringle_1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR0072; CHYMOTRYPSIN.
 DR Prodom; PD00395; Kringle; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00130; EGF; 1.
 DR SMART; SM00020; TRYp_SPC; 1.

Query Match 99.0%; Score 494; DB 1; Length 431;
 Best Local Similarity 98.8%; Pred. No. 8.1e-50;
 Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQQLGKHNHYCRNPDN 60
 Db 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSDALQQLGKHNHYCRNPDN 127

QY 61 RRRPWCVQVQGLKPLVQECMVHDCAD 86
 Db 128 RRRPWCVQVQGLKPLVQECMVHDCAD 153

RESULT 2

UROK_PAPCY STANDARD; PRT; 433 AA.

ID UROK_PAPCY
 AC P16227;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urokinase-type Plasminogen activator precursor (EC 3.4.21.73) (uPA)
 DE (U-plasminogen activator).
 GN PLAU.
 OS Papio cynocephalus (Yellow baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TAXID=9556;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Thoracic aorta;
 RX MEDLINE=90287734; PubMed=2113276;
 RA Au Y.P.T., Wang T.W., Clowes A.W.;
 RT "Nucleotide and deduced amino acid sequences of baboon urokinase-type
 plasminogen activator";
 RL Nucleic Acids Res. 18:3411-3411(1990).
 CC ;- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 -I- SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS
 OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A
 LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 155 IN THE LOW
 MOLECULAR MASS FORM TO YIELD A SHORT ALI CHAIN (BY SIMILARITY).
 -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -I- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

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 or send an email to licensee@isb-sib.ch).

CC EMBL; X51935; CAA36200.1; -.
 DR PIR; S14687; UKBAY.
 DR HSSP; P00749; ILMW.
 DR MEROPS; S01.231; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR001254; Ser_protease_try.
 DR Pfam; PF00051; kringle_1.
 DR Pfam; PF00089; trypsin_1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRODOM; PD000395; Kringle_1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYSPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; FALSE_NEG.
 DR PROSITE; PS00021; KRINGLE_1; 1.

RESULT 3

UROK_PIG STANDARD; PRT; 442 AA.

ID UROK_PIG
 AC P04185;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
 DE (U-plasminogen activator).
 GN PLAU.
 OS Sus scrofa (Pig).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TAXID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85087954; PubMed=6096832;
 RA Nagamine Y., Pearson D., Altus M.S., Reich E.;
 RT "cDNA and gene nucleotide sequence of porcine plasminogen activator.";
 RL Nucleic Acids Res. 12:9525-9541(1984).
 RN [2]
 RP REVISION TO 241.
 RA Nagamine Y.;
 RL Submitted (DEC-1986) to the PIR data bank.
 -I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 -I- Plasminogen to form plasmin.
 -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 -I- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 -I- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Zymogen; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 433
 FT CHAIN 21 176
 FT CHAIN 155 433
 FT CHAIN 178 62
 FT DOMAIN 26 150
 FT DOMAIN 69 177
 FT DOMAIN 151 178
 FT DOMAIN 178 433
 FT DISULFID 30 38
 FT DISULFID 32 50
 FT DISULFID 52 61
 FT DISULFID 167 298
 FT DISULFID 208 224
 FT DISULFID 216 287
 FT DISULFID 315 384
 FT DISULFID 347 363
 FT DISULFID 374 402
 FT ACT_SITE 223 223
 FT ACT_SITE 274 274
 FT ACT_SITE 378 378
 FT CARBOHYD 324 324
 SO SEQUENCE 433 AA; 48595 MW; 816D22DFE0DC8792 CRC64;

Query Match 92.0%; Score 459; DB 1; Length 433;
 Best Local Similarity 93.0%; Pred. No. 9.2e-46;
 Matches 80; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQQLGKHNHYCRNPDN 60
 Db 67 KTCYEGNGHFYRGKASTDTMGRSCLAWNNSATVLQQTYHAHRSDALQQLGKHNHYCRNPDN 127

QY 61 RRRPWCVQVQGLKPLVQECMVHDCAD 86
 Db 127 RRRPWCVQVQGLKPLVQECMVHNCAD 152

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- - - - -

DR EMBL; X01648; CAA25806.1; - .
DR EMBL; X02724; CAA26511.1; - .
DR PIR; A00932; UKPG.
DR HSSP; P00749; IKDU.
DR MEROPS; S01.231; - .
DR InterPro; IPR001314; Chymotrypsin.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00020; TRYPSIN_SPC; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation: Hydrolase; serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 442 BY SIMILARITY.
FT CHAIN 21 188 BY SIMILARITY.
FT CHAIN 190 442 BY SIMILARITY.
FT DOMAIN 29 65 BY SIMILARITY.
FT DOMAIN 72 153 BY SIMILARITY.
FT DOMAIN 154 189 BY SIMILARITY.
FT DOMAIN 190 442 BY SIMILARITY.
FT CARBOHYD 152 152 BY SIMILARITY.
FT DISULFID 33 41 BY SIMILARITY.
FT DISULFID 35 53 BY SIMILARITY.
FT DISULFID 55 64 BY SIMILARITY.
FT DISULFID 179 310 BY SIMILARITY.
FT DISULFID 220 236 BY SIMILARITY.
FT DISULFID 228 299 BY SIMILARITY.
FT DISULFID 324 393 BY SIMILARITY.
FT DISULFID 356 372 BY SIMILARITY.
FT DISULFID 383 411 BY SIMILARITY.
FT ACT_SITE 235 235 BY SIMILARITY.
FT ACT_SITE 286 286 BY SIMILARITY.
FT ACT_SITE 387 387 BY SIMILARITY.
FT CONFLICT 241 241 Q -> H (IN REF. 1; CAA25806).
FT CONFLICT 242 242 Q -> H (IN REF. 1; CAA26511).
FT CONFLICT 288 288 A -> GS (IN REF. 1; CAA25806).
SQ SEQUENCE 442 AA; 49116 MW; EEE32FCEFF501321EE CRC64;

Query Match 82.0%; Score 409; DB 1;
Best Local Similarity 82.4%; Pred. No. 5.8e-40; Length 442;
Matches 70; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

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- - - - -

UROK_RAT
ID UROK_RAT STANDARD; PRT; 432 AA.
AC P29598;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-Plasminogen activator).
GN PLAU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP RC
RA SEQUENCE FROM N.A.
RA STRAIN=Fischer 344;
RX MEDLINE=92233409; PubMed=1568219;
RA Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
RA Kefford R.F.;
RT Transcriptional and posttranscriptional activation of urokinase
RT Plasminogen activator gene expression in metastatic tumor cells.;
RL Cancer Res. 52:2489-2496(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Kidney;
RA Rabbani S.A.;
RA Submitted (APR-1992) to the EMBL/GenBank/DDBJ databases.
- - - CATALYTIC ACTIVITY: Specific cleavage of Arg-1-val bond in
CC Plasminogen to form plasmin.
- - - SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH
CC CONSISTS OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM
CC LOW MOLECULAR MASS FORM TO YIELD A SHORT AL CHAIN (BY SIMILARITY).
CC - - - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC - - - SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC - - - SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
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CC or send an email to license@isb-sib.ch).
- - - - -

DR EMBL; X63434; CAA45028.1; - .
DR EMBL; X65651; CAA46601.1; - .
DR PIR; S18932; S18932.
DR HSSP; P00749; IKDU.
DR MEROPS; S01.231; - .
DR PRODOM; PD000395; Kringle; 1.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR00001; Kringle.
DR InterPro; IPR001254; Ser_protease_Try.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 432 POTENTIAL.
FT CHAIN A (BY SIMILARITY).

FT	CHAIN	180	433	CHAIN B (BY SIMILARITY).
DT	01-JAN-1988	(Rel. 06, Last sequence update)		EGF-LIKE.
DT	15-JUN-2002	(Rel. 41, Last annotation update)		KRINGLE.
DE	urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)			
GN	PLAU.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85179474; PubMed=2985383;			
RA	Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y.,			
RA	Reich E., Kocher H.P., Duvoisin R.M.,			
RT	"Cloning, nucleotide sequencing and expression of cDNAs encoding			
RT	mouse urokinase-type plasminogen activator.";			
FT	Eur. J. Biochem. 148:225-232(1985).			
FT	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88163489; PubMed=2831940;			
RA	Degen S.J.F., Heckel J.L., Reich E., Degen J.L.;			
RT	"The murine urokinase-type plasminogen activator gene."			
RL	Biochemistry 26:8270-8279(1987).			
CC	-!- CATALYTIC ACTIVITY: specific cleavage of Arg-1-val bond in			
CC	plasminogen to form plasmin.			
CC	-!- SUBUNIT: FOUND IN HIGH AND LOW MOLECULAR MASS FORMS. EACH CONSISTS			
CC	OF TWO CHAINS, A AND B. THE HIGH MOLECULAR MASS FORM CONTAINS A			
CC	LONG CHAIN A. CLEAVAGE OCCURS AFTER RESIDUE 156 IN THE LOW			
CC	MOLECULAR MASS FORM TO YIELD A SHORT A1 CHAIN (BY SIMILARITY).			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
CC	-----			
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	DR EMBL; X02389; CAA26231.1; -.			
DR	EMBL; M17922; AAA40539.1; -.			
DR	PIR; A24615; UKMS.			
DR	HSSP; P00749; 1KDU.			
DR	MEROPS; S01.231; -.			
DR	MGD; MGI:9761; Plau.			
DR	InterPro; IPR001314; Chymotrypsin.			
DR	InterPro; IPR000561; EGF-LIKE.			
DR	InterPro; IPR00001; Kringle.			
DR	InterPro; IPR001254; Ser_protease_TRY.			
DR	Pfam; PF00051; kringle; 1.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	ProDom; PD000395; kringle; 1.			
DR	SMART; SM00181; EGF; 1.			
DR	SMART; SM00130; KR; 1.			
DR	SMART; SM0020; TRY_P_SPC; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; FALSE_NEG.			
DR	PROSITE; PS00021; KRINGLE_1; 1.			
DR	PROSITE; PS50070; KRINGLE_2; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
DR	KRingle; EGF-like domain; Zymogen; Signal.			
FT	Kringle; EGF-like domain; Zymogen; Signal.			
FT	SIGNAL			
FT	1 20			
FT	UROKINASE-TYPE PLASMINOGEN ACTIVATOR.			
FT	CHAIN			
FT	21 433			
FT	21 178			
FT	157 178			
CC	-----			
CC	-!- SIMILARITY: MONOMER.			
CC	-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.			
CC	-!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.			
FT	CHAIN	180	433	CHAIN B (BY SIMILARITY).
FT	DOMAIN	28	64	EGF-LIKE.
FT	DOMAIN	71	152	KRINGLE.
FT	DOMAIN	153	179	CONNECTING PEPTIDE.
FT	DISULFID	180	433	SERINE PROTEASE.
FT	DISULFID	32	40	BY SIMILARITY.
FT	DISULFID	34	52	BY SIMILARITY.
FT	DISULFID	54	63	BY SIMILARITY.
FT	DISULFID	169	301	INTERCHAIN (BY SIMILARITY).
FT	DISULFID	211	227	BY SIMILARITY.
FT	DISULFID	219	290	BY SIMILARITY.
FT	DISULFID	315	384	BY SIMILARITY.
FT	DISULFID	347	363	BY SIMILARITY.
FT	DISULFID	374	402	BY SIMILARITY.
FT	ACT_SITE	226	226	CHARGE RELAY SYSTEM.
FT	ACT_SITE	277	277	CHARGE RELAY SYSTEM.
FT	ACT_SITE	378	378	CHARGE RELAY SYSTEM.
FT	SEQUENCE	433 AA;	48268 MW;	A99C35F6250443F9 CRC64;
FT	RESULT	7		
FT	URTB_DESRO			
FT	ID	URTB_DESRO	STANDARD;	PRT; 431 AA.
AC	P98121;			
DT	01-FEB-1996	(Rel. 33, Created)		
DT	01-FEB-1996	(Rel. 33, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Salivary plasminogen activator beta precursor	(EC 3.4.21.68)	(DSPA beta).	(DSPA beta).
DE	Desmodus rotundus (Vampire bat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae; Desmodontinae; Desmodus.			
OC	PIR; A24615; UKMS.			
OC	PIR; A29420; A29420.			
OC	HSSP; P00749; 1KDU.			
OC	MEROPS; S01.231; -.			
OC	DR EMBL; X02389; CAA26231.1; -.			
OC	DR EMBL; M17922; AAA40539.1; -.			
OC	DR PIR; A24615; UKMS.			
OC	DR HSSP; P00749; 1KDU.			
OC	DR MEROPS; S01.231; -.			
OC	DR SMART; SM00181; EGF; 1.			
OC	DR SMART; SM00130; KR; 1.			
OC	DR SMART; SM0020; TRY_P_SPC; 1.			
OC	PROSITE; PS00022; EGF_1; 1.			
OC	PROSITE; PS01186; EGF_2; FALSE_NEG.			
OC	PROSITE; PS00021; KRINGLE_1; 1.			
OC	PROSITE; PS50070; KRINGLE_2; 1.			
OC	PROSITE; PS50240; TRYPSIN_DOM; 1.			
OC	PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.			
OC	PROSITE; PS00135; TRYPSIN_SER; 1.			
OC	Kringle; EGF-like domain; Zymogen; Signal.			
FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	433	UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT	CHAIN	21	178	CHAIN A (BY SIMILARITY).
FT	CHAIN	157	178	SHORT A CHAIN (Al).

DR Pfam; PF00039; fnf; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FNI; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRYSPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS50070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Plasma; Kringle; EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 17 PROBABLE.
 FT PROPEP 18 29
 FT CHAIN 30 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR.
 FT CHAIN 30 308 TISSUE-TYPE PLASMINOGEN ACTIVATOR A
 FT CHAIN 309 559 TISSUE-TYPE PLASMINOGEN ACTIVATOR B
 FT DOMAIN 36 78 CHAIN.
 FT DOMAIN 79 117 FIBRONECTIN.
 FT DOMAIN 124 205 KRINGLE 1.
 FT DOMAIN 213 294 KRINGLE 2.
 FT DOMAIN 309 559 SERINE PROTEASE.
 FT ACT_SITE 355 355 CHARGE RELAY SYSTEM.
 FT ACT_SITE 404 404 CHARGE RELAY SYSTEM.
 FT ACT_SITE 510 510 CHARGE RELAY SYSTEM.
 FT DISULFID 38 68 CATALYTIC ACTIVITY: Specific cleavage of Arg-1-Val bond in
 FT DISULFID 66 75 plasminogen to form plasmin.
 FT DISULFID 83 94 -1- CATALYTIC ACTIVITY: BELONGS TO PEPTIDASE FAMILY S1.
 FT DISULFID 88 105 -1- SUBUNIT: MONOMER.
 FT DISULFID 107 116 -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 FT DISULFID 124 205 CC
 FT DISULFID 145 187 CC
 FT DISULFID 176 200 CC
 FT DISULFID 213 294 CC
 FT DISULFID 234 276 CC
 FT DISULFID 265 289 CC
 FT DISULFID 297 428 CC
 FT DISULFID 340 356 CC
 FT DISULFID 348 417 CC
 FT DISULFID 442 516 CC
 FT DISULFID 474 490 CC
 FT DISULFID 506 534 CC
 FT DISULFID 149 149 CC
 FT CARBOHYD 481 481 CC
 FT CONFLICT 380 380 E -> K (IN REF. 1).
 SQ 559 AA; 62903 MW; 7DBD3809C1D1C921 CRC64;

Query Match 45.3%; Score 226; DB 1; Length 559;
 Best Local Similarity 49.4%; Pred. No. 1.1e-18;
 Matches 41; Conservative 9; Mismatches 33; Indels 0; Gaps 0;

DR Pfam; PF00039; fnf; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYSPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; Signal; Multigene family.
 FT SIGNAL 1 36 POTENTIAL.
 FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
 FT DOMAIN 45 126 KRINGLE.
 FT DOMAIN 142 394 SERINE PROTEASE.
 FT ACT_SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).

AC P49150;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
 DE gamma).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TAXID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat Desmodus rotundus: cloning and expression.";
 RT Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=933393059; PubMed=1309059;
 RX SCHLEUNING W.-D., ALAGON A., BOIDOL W., BRINGMANN P., PETRI T.,
 RA KRAETZSCHMAR J., HAENDLER B., LANGER G., BALDUS B., WITT W.,
 RA DONNER P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RT ANN. N.Y. Acad. Sci. 667:395-403(1992).
 CC -1- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-1-Val bond in
 CC plasminogen to form plasmin.
 CC -1- SIMILARITY: MONOMER.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC
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 CC
 DR EMBL; M63990; AAA31595.1; -.
 DR HSSP; P98119; IAS1.
 DR MEROPS; S01.239; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; Kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYSPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; Signal; Multigene family.
 FT SIGNAL 1 36 POTENTIAL.
 FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
 FT DOMAIN 45 126 KRINGLE.
 FT DOMAIN 142 394 SERINE PROTEASE.
 FT ACT_SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).

RESULT 10
 URTG_DESRO
 ID URTG_DESRO STANDARD; PRT; 394 AA.

FT DISULFID 45 126 BY SIMILARITY.
 FT DISULFID 66 108 BY SIMILARITY.
 FT DISULFID 97 121 BY SIMILARITY.
 FT DISULFID 131 262 BY SIMILARITY.
 FT DISULFID 174 190 BY SIMILARITY.
 FT DISULFID 182 251 BY SIMILARITY.
 FT DISULFID 276 351 BY SIMILARITY.
 FT DISULFID 308 324 BY SIMILARITY.
 FT CARBOHYD 341 369 BY SIMILARITY.
 SO SEQUENCE 315 394 AA: 44105 MW; 9CCD6F52F3D81FCF CRC64;
 Query Match 43.7%; Score 218; DB 1; Length 394;
 Best Local Similarity 45.2%; Pred. No. 6.7e-18;
 Matches 38; Conservative 12; Mismatches 34; Indels 0; Gaps 0;
 QY 2 TCYEGNCHFYRGKASTDTMGRPCLPWNNSATVQLOQVHARNSNALOQIGKHNCRNPDR 61
 ||||: -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -|||
 Db 44 TCYKDQGVYRGTWSTSEGAQCIWNNSNLIRRNTYGRMPEAVKLGIGNHNHYCRNPDGA 103
 QY 62 RRPWCVYVOVGLKPLVQECMVHDCA 85
 :|||||: -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -||| -|||
 Db 104 SKPWCYVIKARKFTSESCSVPVCS 127
 RN RESULT 11
 TPA_HUMAN STANDARD; PRT; 562 AA.
 ID P00750; Q15103; Rel. 01, Created
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
 DE (t-PA) (t-plasminogen activator) (Alteplase).
 GN PLAT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Melanoma;
 RX MEDLINE=83115262; PubMed=6337343;
 RA Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
 RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
 RA Goeddel D.V., Collen D.;
 RT "Cloning and expression of human tissue-type plasminogen activator
 RT cDNA in *E. coli*";
 RL *Nature* 301:214-221(1983).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Fetal lung;
 RX MEDLINE=88262579; PubMed=3133640;
 RA Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
 RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA
 RT from human fetal lung cells";
 RL Nucleic Acids Res. 16:5695-5695(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88054470; PubMed=2824147;
 RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
 RA Hsiung N.;
 RT "Expression of human uterine tissue-type plasminogen activator in
 mouse cells using BPV vectors";
 RL DNA 6:461-472(1987).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86196143; PubMed=3009482;
 RA Friezner Degen S.J., Rajput B., Reich E.;
 RT "The human tissue plasminogen activator gene";
 RL *J. Biol. Chem.* 261:6972-6985(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84298137; PubMed=6089198;
 RA NY T., Elgh F., Lund B.;
 RT "The structure of the human tissue-type plasminogen activator gene:
 RT correlation of intron and exon structures to functional and
 RT structural domains";
 RT PROC. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
 RL [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86284200; PubMed=3090401;
 RA Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.,
 RA Opdenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
 RT "Cloning of cDNA coding for human tissue-type plasminogen activator
 RT and its expression in *Escherichia coli*";
 RL Mol. Biol. Med. 3:279-292(1986).
 RN [7]
 RP SEQUENCE OF 212-361 FROM N.A.
 RX MEDLINE=83169656; PubMed=65572897;
 RA Edlund T., NY T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
 RA Josephson S.;
 RT "Isolation of cDNA sequences coding for a part of human tissue
 RT plasminogen activator";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
 RN [8]
 RP SEQUENCE OF 1-36 FROM N.A.
 RX MEDLINE=85289338; PubMed=3161893;
 RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
 RA Schleuning W.-D.;
 RT "Isolation and characterization of the human tissue-type plasminogen
 RT activator structural gene including its 5' flanking region";
 RL J. Biol. Chem. 260:11223-11230(1985).
 RN [9]
 RP SEQUENCE OF 31-562 FROM N.A.
 RX MEDLINE=91291340; PubMed=1368681;
 RA Itagaki Y., Yasuda T., Mitsuda S., Higashio K.;
 RT "Purification and characterization of tissue plasminogen activator
 RT secreted by human embryonic lung diploid fibroblasts, IMR-90 cells";
 RL Agric. Biol. Chem. 55:1225-1232(1991).
 RN [10]
 RP SEQUENCE OF 36-562.
 RC TISSUE-Melanoma;
 RX MEDLINE=85000468; PubMed=6433976;
 RA Pohl G., Kaelstrom M., Bergsdorf N., Wallen P., Joernvall H.;
 RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
 derived amino acid sequence, identify the active site serine residue,
 RT establish glycosylation sites, and localize variant differences";
 RL Biochemistry 23:3701-3707(1984).
 RN [11]
 RP SEQUENCE OF 33-52 AND 311-330.
 RC TISSUE-Melanoma;
 RX MEDLINE=83209620; PubMed=6682760;
 RA Wallen P., Pohl G., Bergsdorf N., Raanby M., NY T., Joernvall H.;
 RT "Purification and characterization of a melanoma cell plasminogen
 RT activator";
 RL Eur. J. Biochem. 132:681-686(1983).
 RN [12]
 RP SEQUENCE FROM N.A. (SHORT ISOFORM).
 RC TISSUE-Umbilical vein;
 RX MEDLINE=90192129; PubMed=2107528;
 RA Siebert P.D., Fong K.;
 RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
 RT human endothelial cells";
 RL Nucleic Acids Res. 18:1086-1086(1990).
 RN [13]
 RP STRUCTURE OF CARBOHYDRATES;
 RX MEDLINE=90092112; PubMed=2513186;
 RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
 RT "Carbohydrate structure of recombinant human uterine tissue
 RT plasminogen activator expressed in mouse epithelial cells";
 RL Eur. J. Biochem. 186:273-286(1989).
 RN [14]
 RP CARBOHYDRATE-LINKAGE SITE THR-95.
 RX MEDLINE=91159408; PubMed=1900431;
 RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;

RT "Tissue plasminogen activator has an O-linked fucose attached to
 RT threonine-61 in the epidermal growth factor domain.";
 RL Biochemistry 30:2311-2314(1991).
 RN [15]
 RP DISULFIDE BONDS IN KRINGLE 2.
 RX MEDLINE=91244765; PubMed=1645336;
 RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
 RT "disulfide pairing of the recombinant kringle-2 domain of tissue
 plasminogen activator produced in *Escherichia coli*.";
 RL J. Biol. Chem. 266:10070-10072(1991).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
 RX MEDLINE=96200985; PubMed=8613982;
 RA Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
 RA Bode W.;
 RT "The 2.3 Å crystal structure of the catalytic domain of recombinant
 two-chain human tissue-type plasminogen activator.";
 RL J. Mol. Biol. 258:117-135(1996).
 RN [17]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
 RX MEDLINE=97449126; PubMed=9305622;
 RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
 RA Bode W.;
 RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
 crystal structure of single-chain human tPA.";
 RL EMBO J. 16:4797-4805(1997).
 RN [18]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
 RX MEDLINE=92118803; PubMed=1310033;
 RA de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinsky A.,
 RA Westbrook M.L., Kossiakoff A.A.;
 RT "Crystal structure of the kringle 2 domain of tissue plasminogen
 activator at 2.4-Å resolution.";
 RL Biochemistry 31:270-279(1992).
 RN [19]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=90122799; PubMed=2558718;
 RA Byeon I.-J.L., Kelley R.F., Llinas M.;
 RT "1H NMR structural characterization of a recombinant kringle 2 domain
 from human tissue-type plasminogen activator.";
 RL Biochemistry 28:9350-9360(1989).
 RN [20]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=91200042; PubMed=1901789;
 RA Byeon I.-J.L., Kelley R.F., Llinas M.;
 RT "Kringle-2 domain of the tissue-type plasminogen activator. 1H-NMR
 assignments and secondary structure.";
 RL Eur. J. Biochem. 197:155-165(1991).
 RN [21]
 RP STRUCTURE BY NMR OF KRINGLE 2.
 RX MEDLINE=92106329; PubMed=1762144;
 RA Byeon I.-J.L., Llinas M.;
 RT "Solution structure of the tissue-type plasminogen activator kringle
 2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
 drug.";
 RL J. Mol. Biol. 222:1035-1051(1991).
 RN [22]
 RP STRUCTURE BY NMR OF 38-85.
 RX MEDLINE=92292163; PubMed=1602484;
 RA Downing A.K., Driscoll P.C., Harvey T.S., Dudgeon T.J., Smith B.O.,
 RA Baron M., Campbell I.D.;
 RT "Solution structure of the fibrin binding finger domain of
 tissue-type plasminogen activator determined by 1H nuclear magnetic
 resonance";
 RT J. Mol. Biol. 225:821-833(1992).
 RN [23]
 RP STRUCTURE BY NMR OF 36-126.
 RX MEDLINE=96027104; PubMed=7582899;
 RA Smith B.O., Downing A.K., Driscoll P.C., Dudgeon T.J., Campbell I.D.;
 RT "The solution structure and backbone dynamics of the fibronectin type
 I and epidermal growth factor-like pair of modules of tissue-type
 plasminogen activator.";
 RT Structure 3:823-833(1995).

CC -!- FUNCTION: CONVERTS THE ABUNDANT, BUT INACTIVE, ZYMOGEN PLASMINOGEN
 CC TO PLASMIN BY HYDROLYZING A SINGLE ARG-VAL BOND IN PLASMINOGEN. BY
 CC CONTROLLING PLASMIN-MEDIATED PROTEOLYSIS, IT PLAYS AN IMPORTANT
 CC ROLE IN TISSUE REMODELING AND DEGRADATION, IN CELL MIGRATION AND
 CC MANY OTHER PHYSIOPATHOLOGICAL EVENTS.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-| -Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: HETERO-DIMER OF CHAIN A AND CHAIN B HELD BY A DISULFIDE
 CC BOND.
 CC -!- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR.
 CC -!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
 CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
 CC ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
 CC -!- MISCELLANEOUS: BINDS TO THE KRINGLE STRUCTURE OF THE FIBRIN A
 CC CHAIN. BINDING TO FIBRIN ENHANCES ITS CATALYTIC ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 CC
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 CC
 DR EMBL; J03520; AAA40470.1; -.

DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family; 3D-structure.
 FT SIGNAL 1 36 POTENTIAL.
 FT CHAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA_1.
 FT DOMAIN 40 82 FIBRONECTIN TYPE-I.
 FT DOMAIN 83 121 EGF-LIKE.
 FT DOMAIN 128 209 KRINGLE.
 FT DOMAIN 225 477 SERINE PROTEASE.
 FT ACT_SITE 321 321 CHARGE RELAY SYSTEM.
 FT ACT_SITE 428 428 CHARGE RELAY SYSTEM.
 FT DISULFID 70 79 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 92 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 128 209 BY SIMILARITY.
 FT DISULFID 149 191 BY SIMILARITY.
 FT DISULFID 180 204 BY SIMILARITY.
 FT DISULFID 214 345 BY SIMILARITY.
 FT DISULFID 257 273 BY SIMILARITY.
 FT DISULFID 265 334 BY SIMILARITY.
 FT DISULFID 359 434 BY SIMILARITY.
 FT DISULFID 424 452 BY SIMILARITY.
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 398 398 /FTId=CAR_000028.
 SQ SEQUENCE 477 AA; 53616 MW; AA06FD1739C10E5E CRC64;

Query Match 41.7%; Score 208; DB 1; Length 477;
 Best Local Similarity 45.2%; Pred. No. 1.2e-16;
 Matches 38; Conservative 11; Mismatches 35; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQTYHAHRSNALQQLGLKHNHYCRNPNDR 61
 Db 127 TCYEGQGVTYRGTWSTAESRVECINWNSSLTRTRYNGRMPDAFNGLGNGHNYCRNPNGA 186

QY 62 RRPWCYVQVGLKPLVQECMVHDCA 85
 Db 187 PKPWCVVIKAGKFTSECSVVPVCS 210

RESULT 15
 UROK_CHICK ID UROK_CHICK STANDARD; PRT; 434 AA.

AC P15120; DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
 DE (u-plasminogen activator).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE-90110185; PubMed=2295632;
 RA Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;
 RT "The chicken urokinase-type plasminogen activator gene.";
 RL J. Biol. Chem. 265:1339-1344 (1990).
 CC -!- plasminogen to form plasmin.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC ---
 CC DR EMBL; J05187; AAA49131.1;
 CC DR EMBL; J05188; AAA49130.1;
 CC DR PIR; A35005; A35005.
 CC DR HSSP; P00763; 1DPO.
 CC DR MEROPS; S01.231; -.
 CC DR InterPro; IPR001314; Chymotrypsin.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR000001; Kringle.
 CC DR InterPro; IPR001254; Ser_protease_TRY.
 CC DR Pfam; PF00051; kringle; 1.
 CC DR Pfam; PF00089; trypsin; 1.
 CC DR PRINTS; PR0722; CHYMOTRYPSIN.
 CC DR ProDom; PD000395; Kringle; 1.
 CC DR SMART; SM00181; EGF; 1.
 CC DR SMART; SM00130; KR; 1.
 CC DR SMART; SM00020; TRYPSIN_SPC; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS00186; EGF_2; 1.
 CC DR PROSITE; PS00021; KRINGLE_1; 1.
 CC DR PROSITE; PS50070; KRINGLE_2; 1.
 CC DR PROSITE; PS50240; TRYPsin_DOM; 1.
 CC DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE; PS500135; TRYPSIN_SER; 1.
 CC KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 CC KW Kringle; EGF-like domain; Signal; zymogen.
 CC FT SIGNAL 1 20 POTENTIAL.
 CC FT CHAIN 21 434 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
 CC FT CHAIN 21 434 CHAIN A (BY SIMILARITY).
 CC FT DOMAIN 36 72 CHAIN B (BY SIMILARITY).
 CC FT DOMAIN 79 158 KRINGLE.
 CC FT DOMAIN 173 434 CONNECTING PEPTIDE.
 CC FT DISULFID 40 48 SERINE PROTEASE.
 CC FT DISULFID 42 60 BY SIMILARITY.
 CC FT DISULFID 62 71 BY SIMILARITY.
 CC FT DISULFID 162 296 INTERCHAIN (BY SIMILARITY).
 CC FT DISULFID 202 218 BY SIMILARITY.
 CC FT DISULFID 210 285 BY SIMILARITY.
 CC FT DISULFID 310 379 BY SIMILARITY.
 CC FT DISULFID 342 358 BY SIMILARITY.
 CC FT DISULFID 369 397 BY SIMILARITY.
 CC FT ACT_SITE 217 217 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT_SITE 373 373 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 434 AA; 49400 MW; BD881048DD666A55 CRC64;

Query Match 40.8%; Score 203.5; DB 1; Length 434;
 Best Local Similarity 55.9%; Pred. No. 3.5e-16;
 Matches 38; Conservative 6; Mismatches 19; Indels 5; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQ-OTYAHRSNALQQLGLKHNHYCRNPNDR 61
 Db 79 CYSGNGEDYRGMAEDP---GCLYWDHPSVIRWGDYHADLKNALQQLGLKHNHYCRNPNGR 134

QY 62 RRPWCYVQ 69
 Db 135 SRPWCVTK 142

Tue Nov 12 18:06:47 2002

pct-us02-27855-1.rsp

Page 15

Search completed: November 11, 2002, 13:00:25
Job time : 22 secs

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OM protein - protein search, using sw model

Run on: November 11, 2002, 12:24:41 ; Search time 75 Seconds
(without alignments)

236.267 Million cell updates/sec

Title: PCT-US02-27855-1
Perfect score: 499
Sequence: 1 KTCYEGNGHFYRGKASTDTM.....YVQVGLKPLVQECMVHDCAD 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodont:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match Length	DB	ID	Description
1	484	97.0	154	4	Q96SE8	096se8 homo sapien
2	383	76.8	157	6	Q9tva8	Q9tva8 bos taurus
3	306	61.3	214	6	Q9xt70	Q9xt70 orycto ^{la} gus
4	217	43.5	559	11	Q91vp2	Q91vp2 mus musculu
5	216	43.3	395	4	Q9BzW1	Q9bzW1 homo sapien
6	216	43.3	516	4	Q9Bu99	Q9bu99 homo sapien
7	211	42.3	562	6	Q8sq23	Q8sq23 sus scrofa
8	191	38.3	202	13	Q90675	Q90675 gallus gallu
9	188.5	37.8	560	4	Q14520	Q14520 homo sapien
10	188	37.7	653	11	Q8vc54	Q8vc54 mus musculu
11	186.5	37.4	597	11	Q35727	Q35727 mus musculu
12	177.5	35.6	616	6	Q97507	Q97507 sus scrofa
13	157	31.5	452	13	Q90Y90	Q90Y90 xenopus lae
14	153.5	30.8	812	11	Q9r0W3	Q9r0W3 rattus norv
15	153	30.7	454	6	Q46506	Q46506 papio hamad
16	153	30.7	806	6	Q18783	Q18783 macropus eu

ALIGNMENTS

17	152	30.5	113	4	Q9UIR6	Q9uir6 homo sapien
18	151.5	30.4	359	6	Q8WMR1	Q8wmr1 canis famili
19	151	30.3	113	4	Q9UIR7	Q9uir7 homo sapien
20	151	30.3	113	4	Q9UIR5	Q9uir5 homo sapien
21	149	29.9	810	4	Q15146	Q15146 homo sapien
22	148.5	29.8	709	13	Q90ZN6	Q90zn6 brachydano
23	147.5	29.6	399	4	Q96GL8	Q96gl8 homo sapien
24	147.5	29.6	420	4	Q9BTP9	Q9btp9 homo sapien
25	147.5	29.6	716	13	Q91691	Q91691 xenopus lae
26	147	29.5	393	4	Q9BRB6	Q9brb6 homo sapien
27	146	29.3	105	4	Q9UIR8	Q9uir8 homo sapien
28	145	29.1	648	4	Q9H1V4	Q9h1v4 homo sapien
29	144	28.9	567	4	Q13208	Q13208 homo sapien
30	142	28.5	902	5	Q17576	Q17576 caenorhabdi
31	142	28.5	928	5	Q9BLY1	Q9bly1 caenorhabdi
32	139.5	28.0	717	13	P70006	P70006 xenopus lae
33	138	27.7	1145	5	Q9BK18	Q9bk18 aplysia cal
34	137.5	27.6	704	13	Q90865	Q90865 gallus gall
35	137	27.5	812	11	Q91WJ5	Q91wj5 mus musculu
36	135	27.1	132	4	Q16609	Q16609 homo sapien
37	135	27.1	145	6	Q28911	Q28911 macaca fasc
38	134	26.9	685	5	Q24488	Q24488 drosophila
39	133.5	26.8	313	13	Q9PU78	Q9pu78 crocodylus
40	132	26.5	263	4	Q00318	Q00318 homo sapien
41	132	26.5	263	4	Q96FE7	Q96fe7 homo sapien
42	131.5	26.4	215	13	Q42341	Q42341 gallus gall
43	131.5	26.4	716	11	Q91XG8	Q91xg8 mus musculu
44	131.5	26.4	726	13	Q90978	Q90978 gallus gall
45	131.5	26.4	2869	6	Q28398	Q28398 erinaceus e

Query Match 97.0%; Score 484; DB 4; Length 154;
 Best Local Similarity 97.7%; Pred. No. 3.2e-52; Indels 0; Gaps 0;
 Matches 84; Conservative 1; Mismatches 1; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQOPTYHAHRSNALQLGLGKHNCRNPDN 60
 DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQOPTYHAHRSNALQLGLGKHNCRNPDN 127
 RN [1]
 RA SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Vin J., Ideell S.;
 RT "Partial mRNA of rabbit uPA. ";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases
 CC -
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
 CC TRYPSIN FAMILY;
 DR EMBL; AF097647; AAD39351.1; -.
 DR HSSP; P00749; 1EJN.
 DR InterPro; S01.231; -.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR0001314; Chymotrypsin.
 DR InterPro; IPR001254; Ser_Protease_Try.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PRO0722; CHIMOTRYPSIN.
 DR PRODOM; PD000395; kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYPSIN_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR KW Hydrolase; Kinase; Serine protease.
 FT SEQUENCE FROM N.A.
 RX TISSUE=SKELETAL MUSCLE;
 RA MEDLINE=21071388; Pubmed=11204721;
 RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.,
 RT "Coordinate expression of matrix-degrading proteinases and their
 activators and inhibitors in bovine skeletal muscle. ";
 RL J. Anim. Sci. 79:94-107(2001).
 DR EMBL; AF144761; AAD30301.1; -.
 DR HSSP; P00749; 1URK.
 DR MEROPS; S01.231; -.
 DR IPR00051; EGF-like.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00022; EGF_1; EGF-like.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 157 157
 SQ SEQUENCE 157 AA; 17858 MW; A768D6C72C1FBFB7 CRC64;

Query Match 76.8%; Score 383; DB 6; Length 157;
 Best Local Similarity 75.3%; Pred. No. 1.1e-39;
 Matches 64; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQOPTYHAHRSNALQLGLGKHNCRNPDN 60
 DB 36 KTCYQGNHGSYRGKANRDLGRPCLAWDSDPTVLLKMYHAHRSDAIQLGLGKHNCRNPDN 95
 RN [1]
 RA SEQUENCE FROM N.A.
 RC TISSUE=BREAST TUMOR;
 RA Strausberg R.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL; BC011256; AAH11256.1; -.
 DR InterPro; IPR00051; EGF-like.
 DR InterPro; IPR00083; Fibrnctnl.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR001254; Ser_Protease_Try.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fnf; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRODOM; PD000395; Kringle; 2.
 DR SMART; SM00181; Kringle; 2.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.

RESULT 3
 Q9XT70 PRELIMINARY; PRT; 214 AA.
 AC Q9XT70;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Urokinase-type plasminogen activator (Fragment).
 OS Oryctolagus cuniculus (Rabbit).

Query Match 43.3%; Score 216; DB 4; Length 395;
 Best Local Similarity 47.0%; Pred. No. 1.6e-18;
 Matches 39; Conservative 9; Mismatches 35; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVQQLTYAHRSNALQLGLGKHNCRNPDR 62

DB 48 CYFGNGHFSAYRGTHSLTESGASCLPWNNSMILIGKVTAQNPSSAQALGLGKHNCRNPDR 107

DR PROSITE; PS01253; FIBRONECTIN_1; UNKNOWN_1.

DR PROSITE; PS0021; KRINGLE_1; UNKNOWN_2.

DR PROSITE; PS50070; KRINGLE_2; 2.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; UNKNOWN_1.

KW Hydrolase; Serine protease.

SQ SEQUENCE 559 AA; 63122 MW; 8CCEE2BDB94514D9 CRC64;

RESULT 5

Q9BZW1 PRELIMINARY; PRT; 395 AA.

ID Q9BZW1

AC Q9BZW1;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to plasminogen activator, tissue.

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OC [1]

RN [1]

RP RPWCHVMKDRKLITWEYCDMSPCS 295

RA Strausberg, R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.

DR EMBL; AF260825; AAK11956.1; -.

DR HSSP; P0750; 1PK2.

DR MEROPS; S01.232; -.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR00001; Kringle.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00051; kringle; 2.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR PRODOM; PD000395; Kringle; 2.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00130; KR; 2.

DR SMART; SM00020; TRY_SPC; 1.

DR SMART; SM0022; EGF; 1.

DR PROSITE; PS00186; EGF_2; 1.

DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_2.

DR PROSITE; PS50070; KRINGLE_2; 2.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW EGF-like domain; Glycoprotein; Hydrolase; Serine protease.

SQ SEQUENCE 516 AA; 57370 MW; BAB31901FDC96800 CRC64;

RESULT 6

Q9BU99 PRELIMINARY; PRT; 516 AA.

ID Q9BU99

AC Q9BU99;

DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE Similar to plasminogen activator, tissue.

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OC [1]

RP SEQUENCE FROM N.A.

RC TISSUE-SKIN;

RA

RL

CC TRYPSIN FAMILY.

DR EMBL; BC002795; AAH02795.1; -.

DR HSSP; P00750; 1ASH.

DR MEROPS; S01.232; -.

DR InterPro; IPR001314; Chymotrypsin.

DR InterPro; IPR000561; EGF-like.

DR InterPro; IPR00001; Kringle.

DR InterPro; IPR001254; Ser_protease_Try.

DR Pfam; PF00008; EGF; 1.

DR Pfam; PF00051; kringle; 2.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR PRODOM; PD000395; Kringle; 2.

DR SMART; SM00181; EGF; 1.

DR SMART; SM00001; EGF-like; 1.

DR SMART; SM00130; KR; 2.

DR SMART; SM00020; TRY_SPC; 1.

DR SMART; SM0022; EGF; 1.

DR PROSITE; PS00186; EGF_2; 1.

DR PROSITE; PS00021; KRINGLE_1; UNKNOWN_2.

DR PROSITE; PS50070; KRINGLE_2; 2.

DR PROSITE; PS50240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW EGF-like domain; Glycoprotein; Hydrolase; Serine protease.

SQ SEQUENCE 516 AA; 57370 MW; BAB31901FDC96800 CRC64;

RESULT 7

Q8SQ23 PRELIMINARY; PRT; 562 AA.

ID Q8SQ23

AC Q8SQ23;

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)

Db	254	KPWCFIKVNDKVKWEXCDVSACS	277	PRELIMINARY;	PRT;	653 AA.
RESULT	10					
Q8VCS4		PRELIMINARY;	PRT;	653 AA.		
ID	Q8VCS4					
AC	Q8VCS4;					
DT	01-MAR-2002	(TREMBLrel. 20, Created)				
DT	01-MAR-2002	(TREMBLrel. 20, Last sequence update)				
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)				
DE		Hypothetical 70.6 kDa protein.				
OS	Mus musculus (Mouse)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TAXID=10090;					
[1]						
RP	SEQUENCE FROM N.A.					
RC	TISSUE=LIVER;					
RA	Strausberg R.;					
RL	Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.					
DR	EMBL; BC019376; AAH19376.1; -					
DR	InterPro; IPR001314; Chymotrypsin.					
DR	InterPro; IPR00561; EGF-like.					
DR	InterPro; IPR000742; EGF_2.					
DR	InterPro; IPR001438; EGF_II.					
DR	InterPro; IPR00083; Fibronectin.					
DR	InterPro; IPR000562; FN_Type_II.					
DR	InterPro; IPR000001; Kringle.					
DR	InterPro; IPR001254; Ser_protease_Try.					
DR	Pfam; PF00008; EGF; 2.					
DR	Pfam; PF00039; fn1; 1.					
DR	Pfam; PF00040; fn2; 1.					
DR	Pfam; PF00051; kringle; 1.					
DR	Pfam; PF00089; trypsin; 1.					
DR	PRINTS; PR00722; CHYMOTRYPSIN.					
DR	PRINTS; PR00010; EGFBLLOOD.					
DR	PRINTS; PR00013; FNTYPEII.					
DR	PRINTS; PR00018; KRINGLE.					
DR	PRODOM; PD000395; Kringle; 1.					
DR	PRODOM; PD000995; FN_Type_II; 1.					
DR	SMART; SM00181; EGF; 2.					
DR	SMART; SM00058; FN1; 1.					
DR	SMART; SM00059; FN2; 1.					
DR	SMART; SM00130; KR; 1.					
DR	SMART; SM00020; TRY_PSPC; 1.					
DR	PROSITE; PS00022; EGF_1; UNKNOWN_2.					
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.					
DR	PROSITE; PS01253; FIBRONECTIN_1; UNKNOWN_1.					
DR	PROSITE; PS00023; FIBRONECTIN_2; UNKNOWN_1.					
DR	PROSITE; PS00221; KRINGLE_1; UNKNOWN_1.					
DR	PROSITE; PS50070; KRINGLE_2; 1.					
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.					
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.					
DR	PROSITE; PS00135; TRYPSIN_SER; 1.					
DR	PROSITE; PS00136; TRYPSIN_CYS; UNKNOWN_1.					
DR	PROSITE; PS00135; TRYPSIN_HIS; UNKNOWN_1.					
KW	Hypothetical protein.					
SQ	SEQUENCE 653 AA; 70553 MW; FE18D90174ED6FDD CRC64;					
Query	Match	37.7%; Score 188; DB 11; Length 653;				
Best	Local Similarity	53.0%; Pred. No. 8.5e-15;				
Matches	35; Conservative	6; Mismatches 25; Indels 0; Gaps 0;				
Query	3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTYHAHRSNALQLGLGKHNHYCRNPDNRR	60				
Db	283 CFLGNTEVKGAVSTAASGLSCLAWNSDLIYQELHVDSVAAVILGLGPHAYCRNPDKDE	342				
QY	63 RPWCYV 68					
Db	343 RPWCYV 348					
RESULT	12					
QY	2 TCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTY-HAHRSNALQLGLGKHNHYCRNPDN	60				
Db	216 TCYEGRGLSYRGQAGTQSAPCQRW---TVEATYRNMTEKOALSWMGLGHAFCRNPDN	271				
QY	61 RRRPWCYVQVGLKPLVQECMVHDC 84					
Db	272 DTRPWCYVWSGDRLLSDYCGLEQC 295					
RESULT	11					
QY	097507 PRELIMINARY; PRT; 616 AA.					
AC	097507; 01-MAY-1999 (TREMBLrel. 10, Created)					
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)					
RESULT	11					
QY	035727 PRELIMINARY; PRT; 597 AA.					
AC	035727; 01-JAN-1998 (TREMBLrel. 05, Created)					
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	Factor XII.					
GN	F12.					
OS	Mus musculus (Mouse)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TAXID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=LIVER;					
RA	Schloesser M., Schwager S., Engel W.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.					
RL	EMBL; X99571; CAA67891.1; -					
DR	HSSP; P00760; 1AQ7.					
DR	MEROPS; S01.211; -					
DR	MGD; MGI:1891012; F12.					
DR	InterPro; IPR001314; Chymotrypsin.					
DR	InterPro; IPR00561; EGF-like.					
DR	InterPro; IPR000742; EGF_2.					
DR	InterPro; IPR001438; EGF_II.					
DR	InterPro; IPR00083; Fibronectin.					
DR	InterPro; IPR000562; FN_Type_II.					
DR	InterPro; IPR000001; Kringle.					
DR	InterPro; IPR001254; Ser_protease_Try.					
DR	Pfam; PF00088; EGF; 2.					
DR	Pfam; PF00039; fn1; 1.					
DR	Pfam; PF00040; fn2; 1.					
DR	Pfam; PF00051; kringle; 1.					
DR	Pfam; PF00089; trypsin; 1.					
DR	PRINTS; PR00722; CHYMOTRYPSIN.					
DR	PRINTS; PR00018; KRINGLE.					
DR	PRODOM; PD000395; Kringle; 1.					
DR	PRODOM; PD000995; FN_Type_II; 1.					
DR	SMART; SM00181; EGF; 2.					
DR	SMART; SM00058; FN1; 1.					
DR	SMART; SM00059; FN2; 1.					
DR	SMART; SM00130; KR; 1.					
DR	SMART; SM00020; TRY_PSPC; 1.					
DR	PROSITE; PS00022; EGF_1; UNKNOWN_2.					
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.					
DR	PROSITE; PS01253; FIBRONECTIN_1; UNKNOWN_1.					
DR	PROSITE; PS00023; FIBRONECTIN_2; UNKNOWN_1.					
DR	PROSITE; PS00221; KRINGLE_1; UNKNOWN_1.					
DR	PROSITE; PS50070; KRINGLE_2; 1.					
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.					
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.					
DR	PROSITE; PS00135; TRYPSIN_SER; 1.					
KW	EGF-like domain; Glycoprotein; Hydrolase; Serine protease.					
SQ	SEQUENCE 597 AA; 65638 MW; F3AC07C37D0C0FBA_CRC64;					
Query	Match	37.4%; Score 186.5; DB 11; Length 597;				
Best	Local Similarity	44.0%; Pred. No. 1.2e-14;				
Matches	37; Conservative	8; Mismatches 34; Indels 5; Gaps 2;				
QY	2 TCYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQQTY-HAHRSNALQLGLGKHNHYCRNPDN	60				
Db	216 TCYEGRGLSYRGQAGTQSAPCQRW---TVEATYRNMTEKOALSWMGLGHAFCRNPDN	271				
QY	61 RRRPWCYVQVGLKPLVQECMVHDC 84					
Db	272 DTRPWCYVWSGDRLLSDYCGLEQC 295					
RESULT	12					
QY	097507 PRELIMINARY; PRT; 616 AA.					
AC	097507; 01-MAY-1999 (TREMBLrel. 10, Created)					
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)					

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
 DE FXI.
 OS *Sus scrofa* (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Takahashi T.; Kihara T.;
 RT "Porcine liver factor XI.";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL; AB022426; BAA37148.1; -.
 DR HSSP; P00763; 1DPO.
 DR MEROPS; S01.211; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR00561; EGF-like.
 DR InterPro; IPR00742; EGF_2.
 DR InterPro; IPR00083; Fibronectin.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR001254; Ser_protease_try.
 DR Pfam; PF00008; EGF; 2.
 DR Pfam; PF00039; fn1; 1.
 DR Pfam; PF00040; fn2; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPsin.
 DR PRINTS; PR00013; FNTypeII.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 1.
 DR PRODOM; PD000995; FN_Type_II; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00059; FN2; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYPSin; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Glycoprotein; Hydrolase; Serine protease.
 SQ 616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;

Query Match 35.6%; Score 177.5; DB 6; Length 616;
 Best Local Similarity 44.6%; Pred. No. 1.6e-13; Mismatches 37; Conservativeness 6; Matches 35; Indels 5; Gaps 2; Mismatches 35; Indels 5; Gaps 2;

RESULT 14
 Q9R0W3
 ID Q9R0W3
 AC Q9R0W3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Plasminogen protein precursor (EC 3.4.21.7).
 GN PLASMINOGEN.
 OS Rattus norvegicus (Rat).
 OC Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Bangert K.; Johnsen A.H.; Thorsen S.;
 RT "Rat plasminogen: cDNA and gene structure.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.J.; Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor site for plasminogen.";
 RL J. Biol. Chem. 266:10825-10829 (1991).
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL; AU242649; CAB46014.1; -.
 DR HSSP; P00747; 1PMK.
 DR MEROPS; S01.23; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR00001; Kringle.

RESULT 13
 Q90Y90
 ID Q90Y90
 AC Q90Y90;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE KREMEN.
 GN KREMEN.

DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 5.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_PPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 812 AA; 90535 MW; PLASMINOGEN.
 FT SEQUENCE 812 AA; 90535 MW; 8C703C51410EBC9E CRC64;

Query Match 30.8%; Score 153.5; DB 11; Length 812;
 Best Local Similarity 38.9%; Pred. No. 2.1e-10; Gaps 6;
 Matches 35; Conservative 13; Mismatches 27; Indels 15; Gaps 6;

Qy 3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQO-QTYHAHRSNALQQLGLGKHNHYCRNPD 59
 Db 376 CYQNGNGKSYRGTTSSTNTGKKCQSW----VSMTPHSHSKTPANFPDAGL-EMNYCERNPD 429

Qy 60 N-RRRPWCYVQVGLKPLV--QECMVHDCAD 86
 Db 430 NDQRGPWCF---TDPSVRYEYCNLKRSE 456

Search completed: November 11, 2002, 13:01:56
 Job time : 78 secs

DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS50070; KRINGLE_2; 2.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Lipoprotein; Serine protease.

FT NON_TER 1 1
 SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;
 Query Match 30.7%; Score 153; DB 6; Length 454;
 Best Local Similarity 38.6%; Pred. No. 1.2e-10; Gaps 4;
 Matches 34; Conservative 11; Mismatches 31; Indels 12; Gaps 4;

Qy 3 CYEGNGHFYRGKASTDTMGRPCLPWNNSATVLQO-QTYHAHRSNALQQLGLGKHNHYCRNPD 60
 Db 102 CYHGDGQSYRGSFSITVTGRTCSQSSMTPHQHKRTPENHPNDGTM----NYCRNPD 156

Qy 61 RRRPWCYVQVGLKPLV--QECMVHDCAD 86
 Db 157 DTGPWCFT---MDPSYRWEYCNLTRCSD 181

RESULT 15

046506 ID 046506 PRELIMINARY; PRT; 454 AA.
 AC 046506;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAPOA.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox L.A., Jett C., Hixson J.E.;
 RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation Is Associated with Deletion of a Single Exon in a Null RT Allele.";
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC - SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
 DR EMBL; AF029691; AAB97886.1; -.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.226; -.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRY_PPC; 1.

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OM nucleic - nucleic search, using sw model

SUMMARIES

Run on: November 11, 2002, 11:35:58 ; Search time 2622 Seconds
(without alignments)
2863.663 Million cell updates/sec

Title: PCT-US02-27855-2
Perfect score: 258
Sequence: 1 aaaaacctgtatgagggaa.....tggtgcatgactgcgcagat 258

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_v1: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_v1: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pln: *
35: em_htg_rod: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query	Match %	Length	DB ID	Description
1	256.4	99.4	423	6	A76865	A76865 Sequence 3
2	256.4	99.4	1236	6	E02578	E02578 DNA encodin
3	256.4	99.4	1236	6	E02579	E02579 Human prour
4	256.4	99.4	1236	6	E02708	E02708 DNA sequenc
5	256.4	99.4	1236	6	E02709	E02709 DNA sequenc
6	256.4	99.4	1236	6	E02710	E02710 DNA sequenc
7	256.4	99.4	1236	6	E02832	E02832 DNA encodin
8	256.4	99.4	1236	6	E02833	E02833 DNA encodin
9	256.4	99.4	1296	6	E02577	E02577 DNA encodin
10	256.4	99.4	1296	6	E02647	E02647 DNA sequenc
11	256.4	99.4	1296	6	E02649	E02649 DNA sequenc
12	256.4	99.4	1296	6	E02711	E02711 DNA sequenc
13	256.4	99.4	1296	6	E06064	E06064 DNA encodin
14	256.4	99.4	1359	6	AX451990	AX451990 Sequence
15	256.4	99.4	1394	6	E00421	E0421 cDNA coding
16	256.4	99.4	1474	6	E02095	E02095 DNA sequenc
17	256.4	99.4	1474	6	E00924	E00924 cDNA encodin
18	256.4	99.4	1474	6	E01559	E01559 cDNA sequen
19	256.4	99.4	1474	6	E01580	E01580 cDNA encodin
20	256.4	99.4	1474	6	E02114	E02114 cDNA sequenc
21	256.4	99.4	1475	6	AX365729	AX365729 Sequence
22	256.4	99.4	1475	6	E01560	E01560 cDNA sequen
23	256.4	99.4	1475	9	HUMUKM1	K03226 Human prepr
24	256.4	99.4	1964	6	A18397	A18397 Human upA c
25	256.4	99.4	1964	6	AX402384	AX402384 Sequence
26	256.4	99.4	1964	6	AX451989	AX451989 Sequence
27	256.4	99.4	2293	6	A11978	A11978 Synthetic
28	256.4	99.4	2294	6	A09202	A09202 Artificial
29	256.4	99.4	2294	6	AX365730	AX365730 Sequence
30	256.4	99.4	2294	9	HUMUKA	D00244 Homo sapien
31	256.4	99.4	2294	11	G27040	G27040 SHGC-31374
32	256.4	99.4	2296	6	A35395	A35395 H. sapiens u
33	256.4	99.4	2300	6	A04029	A04029 Synthetic H
34	256.4	99.4	2300	6	A21571	A21571 Pro-Urokinase
35	256.4	99.4	2301	6	E01467	E01467 DNA encodin
36	256.4	99.4	2303	6	I07013	I07013 Sequence 4
37	256.4	99.4	2303	6	I08092	I08092 Sequence 1
38	256.4	99.4	2304	6	E00178	E00178 cDNA encod1
39	256.4	99.4	2304	6	I03932	I03932 Sequence 6
40	256.4	99.4	2304	6	I04632	I04632 Sequence 1
41	256.4	99.4	2304	9	HUMUKPM	M15476 Human pro-u
42	256.4	99.4	2345	9	BC013575	BC013575 Homo sapi
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44	256.4	99.4	10332	6	A83180	A83180 Sequence 13
45	256.4	98.8	473	9	AY029537	AY029537 Homo sapi

ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a

RESULT 1
A76865
LOCUS A76865 423 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 3 from Patent WO9315199.
ACCESSION A76865
VERSION A76865.1 GI:6088666
KEYWORDS SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 423)
AUTHORS Fleer, R. and Fournier, A.
TITLE NOVEL BILOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
Patent: WO 9315199-A 3 05-AUG-1993;
JOURNAL

Db 142 AAAACCTGCTATCAGGGGAATGGTCAC'TTACCGAGGAAGGCCAGCACTGACACCATG 201
 Qy 61 GGCGGGCCCTGCCCTGCCACTCTGCCACTGTCCTTCAGCAAACGTACCATGCCAC 120
 Db 202 GGCGGGCCCTGCCCTGCCACTCTGCCACTGTCCTTCAGCAAACGTACCATGCCAC 261
 Qy 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACGACAC 180
 Db 262 AGATCTGATGCTCTCAGTGGGCTGGGAAACATAATTACTGCAGGAACGACAC 321
 Qy 181 CGGAGGGACCCCTGGTCTATGTGCAGGTTGGCCTAAAGCCGCTGTCCAAAGAGTGCATG 240
 Db 322 CGGAGGGACCCCTGGTCTATGTGCAGGTTGGCCTAAAGCCGCTGTCCAAAGAGTGCATG 381
 Qy 241 GTGCATGACTGCCAGAT 258
 Db 382 GTGCATGACTGCCAGAT 399

RESULT 6

LOCUS E02710 1236 bp DNA sequence coding for prourokinase derivative, UK-S3.
 DEFINITION DNA sequence coding for prourokinase derivative, UK-S3.
 ACCESSION E02710
 VERSION E02710.1
 KEYWORDS GI:2170938
 SOURCE JP 1991022979-A/3.
 ORGANISM Unidentified.
 REFERENCE 1. (bases 1 to 1236)
 AUTHORS Yasumura,S., Nishi,T. and Itoh,S.
 TITLE NOVEL PLASMINOGEN-ACTIVATION FACTOR
 JOURNAL PATENT: JP 1991022979-A 3 31-JAN-1991;
 COMMENT KYOWA HAKKO KOGYO CO LTD
 PD 31-JAN-1991
 PF 19-JUN-1989 JP 1989156302
 PI YASUMURA SHIGEYOSHI, NISHI TATSUYA, ITOU SEIGA PC
 C12N9/72, C12N15/58, (C12N9/72, C12R1:19);
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 CC *source: library=plasmid PUKS3;
 FH Key Location/Qualifiers
 FT CDS 1..1236
 FT /product='Prourokinase derivative, UK-S3' FT
 FT modified_base 457. .459 /note='ctg' is replaced by 'aat' FT
 FT modified_base 463. .465 /note='ccc' is replaced by 'acg' .
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 /organism="Hepatitis B virus"
 /db_xref="taxon:10407"
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Query Match 99.4%; Score 256.4; DB 6; Length 1236;
 Best Local Similarity 99.6%; Pred. No. 1.6e-66;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 252 AGATCTGATGCTCTCAGCTGGCCCTGGGAACATAATTACTGCAGGACCCAGACAC 321
 Qy 181 CGGAGGGACCCCTGGTCTATGTGCAGGTTGGCCTAAAGCCGCTTGTCAGAGTGCATG 240
 Db 322 CGGAGGGACCCCTGGTCTATGTGCAGGTTGGCCTAAAGCCGCTTGTCAGAGTGCATG 381
 Qy 241 GTGCATGACTGCCAGAT 258
 Db 382 GTGCATGACTGCCAGAT 399

RESULT 7

LOCUS E02832 1236 bp RNA linear PAT 29-SEP-1997
 DEFINITION DNA encoding human pro-urokinase.
 ACCESSION E02832
 VERSION E02832.1
 KEYWORDS JP 1991087180-A/1.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 REFERENCE 1. (bases 1 to 1236)
 AUTHORS Tanabe,T., Amatsuji,Y., Kasai,S., Hirose,M., Morita,M., Kawabe,H. and Arimura,H.
 TITLE MUTANT HUMAN-PROUROKINASE, ITS PRODUCTION, DNA SEQUENCE, PLASMID AND HOST
 JOURNAL Patent: JP 1991087180-A 1 11-APR-1991;
 COMMENT GREEN CROSS CORP:THE OS Homo sapiens (human)
 PN JP 1991087180-A/1
 PD 11-APR-1991
 PF 16-FEB-1990 JP 1990036809
 PR 18-MAY-1989 JP 89P 126434
 PI TANABE TOSHIKUMI, AMATSUJI YASUO, KASAI SHUNJI, HIROSE MASAHI, PI MORITA MASANORI, KAWABE HARUHIDE, ARIMURA HIROBUMI PC C12N9/72,C12N5/10,C12N15/58;
 CC strandedness: Double;
 CC topology: Linear;
 CC hypothetical: No;
 CC anti-sense: No;
 FH Key Location/Qualifiers
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 FT /product='Prourokinase derivative, UK-S3' FT
 FT mat_peptide 1..1233 /product='pro-urokinase'
 FT /product='pro-urokinase'
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 Best Local Similarity 99.6%; Pred. No. 1.6e-66;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 142 AAAACCTGCTATGAGGGGAATGGTCAC'TTACCGAGGAAGGCCAGCACTGACACCATG 60
 Qy 61 GGCGGGCCCTGCCCTGCCACTCTGCCACTGTCCTTCAGCAAACGTACCATGCCAC 120
 Db 202 GGCGGGCCCTGCCCTGCCACTCTGCCACTGTCCTTCAGCAAACGTACCATGCCAC 261
 Qy 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGACCCAGACAC 180
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Qy	121	AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAAC	180
Db	262	AGATCTGATGCTCTTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAAC	321
Qy	181	CGGAGGCCACCTGGTGTATGTGCAGGTGGCCTAAGCCCTGTCAAGAGTGCATG	240
Db	322	CGGAGGCCACCTGGTGTATGTGCAGGTGGCCTAAGCCCTGTCAAGAGTGCATG	381
Qy	241	GTGCATGACTGCCAGAT	258
Db	382	GTGCATGACTGCCAGAT	399
RESULT 8			
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LOCUS	E02833	1236 bp	RNA
DEFINITION		DNA encoding human pro-urokinase.	linear
ACCESSION	E02833		PAT 29-SEP-1997
VERSION	E02833.1	GI:2171061	
KEYWORDS		JP 1991087181-A/1.	
SOURCE		Homo sapiens.	
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1 (bases 1 to 1236)	
AUTHORS		Tanabe, T., Amatsuji, Y., Kasai, S., Hirose, M., Morita, M., Kawabe, H. and Arimura, H.	
TITLE		MUTANT HUMAN-PROUROKINASE, ITS PRODUCTION, DNA SEQUENCE, PLASMID AND HOST	
JOURNAL		PATENT: JP 1991087181-A 1 11-APR-1991;	
COMMENT		GREEN CROSS CORP:THE	
OS		Homo sapiens (human)	
PN		JP 1991087181-A/1	
PD		11-APR-1991	
PF		22-FEB-1990 JP 1990042020	
PR		18-MAY-1989 JP 89P 126433	
PI		TANABE TOSHIKUMI, AMATSUJI YASUO, KASAI SHUNJI, HIROSE MASAHI, PI MORITA MASANORI, KAWABE HARUHIDE, ARTMURA HIROBUMI PC C12N9/72,C12N5/10,C12N15/58;	
CC		strandness: Double;	
CC		topology: Linear;	
CC		hypothetical: No;	
CC		anti-sense: No;	
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Best Local Similarity		99.6%	Pred. No. 1.6e-66;
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Best Local Similarity		99.6%	Pred. No. 1.6e-66;
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BASE COUNT	327	a 361 c 337 g 271 t	
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Best Local Similarity		99.6%	Pred. No. 1.6e-66;
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Qy	121	AGATCTAATGCTCTCAGCTGGGCTGGGAACATAATTACTGCAGGAACCCAGACAAC	180	Qy	241	GTGCATGACTGCGCAGAT	258
Db	322	AGATCTGCTCTCAGCTGGGCTGGGAACATAATTACTGCAGGAACCCAGACAAC	381	Db	442	GTGCATGACTGCGCAGAT	459
Qy	181	CGGAGGGACCCCTGGTCTATGCGAGGTGGCTAAAGCCGCTTGTCAGAGTCATG	240	RESULT	11		
Db	382	CGGAGGGACCCCTGGTCTATGCGAGGTGGCTAAAGCCGCTTGTCAGAGTCATG	441	LOCUS	E02649		
Qy	241	GTGCATGACTGCGCAGAT	258	DEFINITION	E02649	1296 bp	DNA
Db	442	GTGCATGACTGCGCAGAT	459	ACCESSION	E02649	sequence coding for human pro-urokinase.	
Qy	442	GTGCATGACTGCGCAGAT	459	VERSION	E02649.1	GI:2170877	
Db				KEYWORDS			
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				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
				Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
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				1		linear	PAT 29-SEP-1997
				DEFINITION			
				DNA sequence coding for pro-urokinase.			
				ACCESSION			
				E02647			
				VERSION			
				E02647.1			
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				KYOWA HAKKO KOGYO CO LTD, JITSUKEN DOBUTSU CHUO KENKYUSHO			
				OS			
				Homo sapiens (human)			
				PN			
				JP			
				PD			
				24-OCT-1990			
				PF			
				31-MAR-1989			
				JP			
				PI			
				SEKINE SUSUMU, ITOU SEIGA, KATSUKI MOTOYA			
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				C12N5/85, A01K67/027, C12N1/21, C12N9/72/C12N15/58, (C12N1/21,			
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				C12R1:19);			
				CC			
				strandedness: Double;			
				CC			
				hypothesical: Linear;			
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				anti-sense: No;			
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				Query Match			
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				Best Local Similarity 99.4%; Pred. No. 1.6e-66;			
				Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
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				60			
				Db			
				202 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCCACTGACACCATG			
				261			
				QY			
				61			
				GGCGGGCCCTGCCTGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC			
				120			
				Db			
				262 GGCGGGCCCTGCCTGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC			
				321			
				QY			
				121			
				AGATCTAATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC			
				180			
				Db			
				382 CGGAGGGACCCCTGGCTATGTCAGGTGGCCTAAAGCCGCTTGTCAGAGTCATG			
				441			
				QY			
				181 CGGAGGGACCCCTGGCTATGTCAGGTGGCCTAAAGCCGCTTGTCAGAGTCATG			
				240			
				Db			
				442 GTGCATGACTGCGCAGAT			
				459			
				RESULT			
				12			
				LOCUS			
				E02711			
				1296 bp			
				DNA			
				linear			
				PAT 29-SEP-1997			

DEFINITION DNA sequence coding for native prourokinase.

ACCESSION E02711

VERSION E02711.1

KEYWORDS GI:2170939

SOURCE Unidentified.

ORGANISM Hepatitis B virus

Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.

REFERENCE 1 (bases 1 to 1296)

AUTHORS Yasumura, S., Nishi, T. and Ito, S.

JOURNAL NOVEL PLASMINOGEN-ACTIVATION FACTOR

Patent: JP 1991022979-A 31-JAN-1991;

KYOWA HAKKO KOGYO CO LTD

PN JP 1991022979-A/4

PD 31-JAN-1991

PF 19-JUN-1989 JP 1989156302

PT YASUMURA SHIGEYOSHI, NISHI TATSUYA, ITOU SEIGA PC

C12N9/72, C12N15/58, (C12N9/72, C12R1:19);

CC strandedness: Double;

CC topology: Linear;

CC hypothetical: No;

CC anti-sense: No;

FH Key Location/Qualifiers

FT sig_peptide 1. .60

FT CDS /product='Native prourokinase signal peptide'

FT 61. .1296

FT /product='Native prourokinase' FT

FT mat_peptide 61. .192

FT /note='Growth factor domain'

FT mat_peptide 193. .459

FT /note='tarningul domain'

FT mat_peptide 460. .1293

FT /note='Protease domain'.

FEATURES source

1. .1296

/organism="Hepatitis B virus"

BASE COUNT 327 a 361 c 337 g 271 t

ORIGIN

Query Match 99.4%; Score 256.4; DB 6; Length 1296;

Best Local Similarity 99.6%; Pred. No. 1.6e-66;

Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACTGACACCATG 60

Db 202 AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACTGACACCATG 261

QY 61 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGTCTTACCGAGGAAGGCCAGCACTGACACCATG 120

Db 262 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGTCTTACCGAGGAAGGCCAGCACTGACACCATG 321

QY 121 AGATCTAATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180

Db 322 AGATCTGATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 381

QY 181 CGGAGGGGACCCCTGGTCTATGTGCAGGTGGCCTAAAGCCCTGTCCAAAGAGTCATG 240

Db 382 CGGAGGGGACCCCTGGTCTATGTGCAGGTGGCCTAAAGCCCTGTCCAAAGAGTCATG 441

QY 241 GTGCATGACTGCGCAGAT 258

Db 442 GTGCATGACTGCGCAGAT 459

RESULT 13

E06064 E06064 1296 bp RNA linear PAT 29-SEP-1997

LOCUS DNA encoding human urokinase.

DEFINITION

ACCESSION E06064

VERSION E06064.1 GI:2174251

KEYWORDS Homo sapiens

SOURCE human.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

COMMENT

REFERENCE 1 (bases 1 to 1296)

AUTHORS Yasumura, S., Yamamoto, Y., Hasegawa, M., Higo, K., Kubo, K. and Kuwabara, T.

JOURNAL HUMAN PROUROKINASE DERIVATIVE

PATENT: JP 199336965-A 2 21-DEC-1993;

KYOWA HAKKO KOGYO CO LTD

OS Homo sapiens (human)

PN JP 199336965-A/2

PD 21-DEC-1993

PF 17-OCT-1991 JP 1991269615

PI YASUMURA SHIGEYOSHI, YAMAMOTO YOSHINORI, HASEGAWA MAMORU, PI

HIGO KATSUYA, KUBO KAZUHIRO, KUWABARA TAKASHI

PC C12N9/72, C12N1/21, C12N15/58;

CC strandedness: Double;

CC topology: Linear;

CC *source: strain=Detroit562;

CC *source: clone=puK1, puK11;

FH Key Location/Qualifiers

FT CDS

FT 1. .1296

FT /product='human prourokinase' FT sig_peptide

FT 1. .60

FT mutation replace(88. .195, '')

FT mutation /note='UK-deltaGS1'

FT mutation replace(540. .541, 'aa')

FT mutation /note='UK-deltaGS1'.

FEATURES source

1. .1296

/organism="Homo sapiens"

BASE COUNT 327 a 361 c 337 g 271 t

ORIGIN

Query Match 99.4%; Score 256.4; DB 6; Length 1296;

Best Local Similarity 99.6%; Pred. No. 1.6e-66;

Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60

Db 202 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 261

QY 61 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGTCTTACCGAGGAAGGCCAGCACTGACACCATG 120

Db 262 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGTCTTACCGAGGAAGGCCAGCACTGACACCATG 321

QY 121 AGATCTAATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180

Db 322 AGATCTGATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 381

QY 181 CGGAGGGGACCCCTGGTCTATGTGCAGGTGGCCTAAAGCCCTGTCCAAAGAGTCATG 240

Db 382 CGGAGGGGACCCCTGGTCTATGTGCAGGTGGCCTAAAGCCCTGTCCAAAGAGTCATG 441

QY 241 GTGCATGACTGCGCAGAT 258

Db 442 GTGCATGACTGCGCAGAT 459

RESULT 14

AX451990 AX451990 1359 bp DNA linear PAT 06-JUL-2002

LOCUS AX451990

DEFINITION Sequence 3 from Patent WO0244393.

ACCESSION AX451990

VERSION AX451990.1 GI:21711991

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

SOURCE Homo sapiens

REFERENCE	1	FT	sig_peptide	1. . 60	
AUTHORS	Armendariz Borunda, J. and Aguilar Cordova, E.	FT	mat_peptide	61. .1296	
TITLE	Recombinant viral and non-viral vectors containing the human urokinase plasminogen activator gene and its utilization in the treatment of various types of hepatic, renal, pulmonary, pancreatic and cardiac fibrosis and hypertrophic scars	FT	/Product-'urokinase'	1. .1296.	
JOURNAL	Patent: WO 0244393-A 3 06-JUN-2002;	FT	CDS	Location/Qualifiers	
FEATURES	TGT LAB S A DE C V (MX)	FEATURES	1. .1394	1. .1394	
source	Location/Qualifiers	source	/organism="Homo sapiens"	/organism="Homo sapiens"	
BASE COUNT	358	BASE COUNT	/db_xref="taxon:9606"	/db_xref="taxon:9606"	
ORIGIN	a	ORIGIN	/db_xref="taxon:9606"	/db_xref="taxon:9606"	
Query Match	99.4%	Query Match	99.4%	Query Match	99.4%
Best Local Similarity	99.6%	Pred. No.	1.6e-66	Best Local Similarity	99.6%
Matches	257;	Mismatches	0;	Matches	257;
Db	228	Db	202	Db	202
Qy	1	Qy	1	Qy	1
Db	61	Db	61	Db	61
Qy	61	Db	262	Db	262
Db	288	Qy	121	Db	322
Qy	121	Db	382	Qy	181
Db	348	Qy	180	Db	382
Qy	181	Db	407	Qy	180
Db	408	Qy	467	Db	442
Qy	241	Db	467	Qy	241
Db	468	Qy	485	Db	459
RESULT	15	Search completed: November 11, 2002, 12:24:38	Job time : 2627 secs	RESULT	15
E00421	E00421	1394 bp RNA	linear	PAT	29-SEP-1997
LOCUS	LOCUS	CDNA	coding	CDNA	coding
DEFINITION	urokinase and its flanking region.	urokinase	urokinase	urokinase	urokinase
ACCESSION	E00421	line	region.	line	region.
VERSION	E00421.1	PAT	29-SEP-1997	PAT	29-SEP-1997
KEYWORDS	GI:2168704	29-SEP-1997		29-SEP-1997	
SOURCE	JP 1985180591-A/1.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 1394)				
AUTHORS	Hiramatsu, T., Kaneda, T., Nagai, M., Arimura, H., Nishida, M. and Suyama, T.				
TITLE	DNA SEQUENCE, PLASMID AND HOST OF HUMAN UROKINASE				
JOURNAL	Patent: JP 1985180591-A 1 14-SEP-1985;				
COMMENT	GREEN CROSS CORP: THE				
OS	Homo sapiens (Human)				
PN	JP 1985180591-A/1				
PD	14-SEP-1985				
PF	27-FEB-1984				
PI	HIRAMATSU TAKASHI, KANEDA TERUO, NAGAI MASANORI, PI ARIMURA HIROBUMI, NISHIDA MASAYUKI, SUYAMA TADAKAZU				
PC	C12N15/00, C07H21/04, C12N1/00, C12N9/72, C12N1/00, C12R1:19; CC				
CC	strandedness: Double;				
CC	topology: Linear;				
CC	hypothetical: No;				
CC	anti-sense: No;				
CC	*source: tissue_type=kidney;				
CC	Feature is identified by similarity;				
FH	key	Location/Qualifiers			

PR 20-JUN-2000; 2000US-212874P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Cines DB, Higazi AA;
 XX
 DR WPI; 2002-122240/16.
 XX
 PT P-PSDB; AAE16542.
 PT Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 PT comprising domains from urokinase-type plasminogen activator -
 XX
 PS Claim 29; Fig 1J; 117pp; English.
 XX
 CC The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is a human urokinase-type plasminogen activator (uPA) kringle
 CC DNA.
 XX
 SQ Sequence 264 BP; 66 A; 74 C; 74 G; 50 T; 0 other;
 CC Query Match 99.4%; Score 256.4; DB 24; Length 264;
 CC Best Local Similarity 99.6%; Pred. No. 1.4e-34;
 CC Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACTGACACCATG 60
 DB 1 AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACTGACACCATG 60
 CC
 QY 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 DB 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 CC
 QY 121 AGATCTAATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 DB 121 AGATCTAATGCTCTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 CC
 QY 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 DB 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 CC
 QY 241 GTGCATGACTGCGCAGAT 258
 DB 241 GTGCATGACTGCGCAGAT 258
 XX
 SQ Sequence 288 BP; 73 A; 84 C; 77 G; 54 T; 0 other;
 CC Query Match 99.4%; Score 256.4; DB 24; Length 288;
 CC Best Local Similarity 99.6%; Pred. No. 1.4e-34;
 CC Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
 DB 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
 CC
 QY 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 DB 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 CC
 QY 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 DB 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 CC
 QY 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 DB 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 CC
 QY 241 GTGCATGACTGCGCAGAT 258
 DB 241 GTGCATGACTGCGCAGAT 258

KW adult respiratory distress syndrome; male impotence; ds.
 XX
 OS Homo sapiens.
 XX
 KEY
 FH
 FT
 CDS
 FT
 FT
 FT
 FT
 FT
 FT
 PN WO200197752-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-US18976.
 XX
 PR 20-JUN-2000; 2000US-212874P.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 XX
 PI Cines DB, Higazi AA;
 XX
 DR WPI; 2002-122240/16.
 XX
 PT P-PSDB; AAE16550.
 XX
 PT Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 PT comprising domains from urokinase-type plasminogen activator -
 XX
 PS Claim 29; Fig 1R; 117pp; English.
 XX
 CC The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is a DNA encoding human urokinase-type plasminogen activator
 CC (uPA) kringle and connecting peptide.
 XX
 SQ Sequence 288 BP; 73 A; 84 C; 77 G; 54 T; 0 other;
 CC Query Match 99.4%; Score 256.4; DB 24; Length 288;
 CC Best Local Similarity 99.6%; Pred. No. 1.4e-34;
 CC Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
 DB 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
 CC
 QY 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 DB 61 GGCGGGCCCTGGCTGCCCCTGGAACTCTGCCACTGTCCCTCAGCAACGTACCATGCCAC 120
 CC
 QY 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 DB 121 AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC 180
 CC
 QY 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 DB 181 CGGAGGCACCTCTGGTGCATGTGCAAGAGTCATG 240
 CC
 QY 241 GTGCATGACTGCGCAGAT 258
 DB 241 GTGCATGACTGCGCAGAT 258

RESULT 3

ID AAD27078 standard; DNA; 405 BP.

AC AAD27078;

XX 09-APR-2002 (first entry)

DE Human urokinase-type plasminogen activator amino terminal fragment DNA.

XX Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..405

FT /*tag= a /product= "Human uPA ATF"

FT /note= "CDS does not include start and stop codon"

FT /partial

PN WO200197752-A2.

XX 27-DEC-2001.

XX 13-JUN-2001; 2001WO-US18976.

PR 20-JUN-2000; 2000US-212874P.

PA <UYPE-> UNIV PENNSYLVANIA.

XX PT Cines DB, Higazi AA;

XX DR WPI; 2002-122240/16.

XX DR P-PSDB; AAE16545.

PT Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator -

PT Claim 29; Fig 1M; 117pp; English.

XX The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular occlusions, thrombotic microangiopathies, surgically induced thrombotic disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma, diabetic retinopathy, wound healing, clotting disorder, uterine contraction disorder, male impotence, respiratory disease or condition such as asthma, adult respiratory distress syndrome, primary pulmonary hypertension, microvascular thrombotic occlusion, and a disorder associated with chronic intrapulmonary fibrin formation. The present sequence is human urokinase-type plasminogen activator (uPA) amino terminal fragment (ATF) DNA.

XX Sequence 405 BP; 113 A; 104 G; 83 T; 0 other;

Query Match 99 4%; Score 256.4; DB 24; Length 405;

Best Local Similarity 99.6%; Pred. No. 1.3e-34;

Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAACTGGTCACTTTACCGAGGAAGGCCAGTACGACACCATG

Db 142 AAAACCTGCTATGAGGGAACTGGTCACTTTACCGAGGAAGGCCAGTACGACACCATG 201

QY 61 GCGCGGCCCTGCCCTGGAACTCTGCCACTGTCTTCAGCAACGTTACCATGCCAC 120

Db 202 GCGCGGCCCTGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTTACCATGCCAC 261

QY 121 AGATCTAATGCTCTTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180

Db 262 AGATCTGATGCTCTTCAGCTGGGAAACATAATTACTGCAGGAACCCAGACAC 321

QY 181 CGGAGGGGACCCCTGGTGTATGTCAGGGGGCTAAAGCCGCTGTCCAAGAGTGCATG 240

Db 322 CGGAGGGGACCCCTGGTGTATGTCAGGGTGGCCTAAAGCCGCTGTCCAAGAGTGCATG 381

QY 241 GTGCATGACTGCCAGAT 258

Db 382 GTGCATGACTGCCAGAT 399

RESULT 4

ID AAD27082 standard; DNA; 429 BP.

AC AAD27082;

XX 09-APR-2002 (first entry)

DE Human uPA amino terminal fragment (ATF) and connecting Peptide DNA.

XX Human; urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; ATF; male impotence; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..429

FT /*tag= a /product= "Human uPA ATF and connecting peptide"

FT /note= "CDS does not include start and stop codon"

FT /partial

PN WO200197752-A2.

XX 27-DEC-2001.

XX 13-JUN-2001; 2001WO-US18976.

PR 20-JUN-2000; 2000US-212874P.

PA <UYPE-> UNIV PENNSYLVANIA.

XX PT Cines DB, Higazi AA;

XX DR WPI; 2002-122240/16.

XX DR P-PSDB; AAE16549.

PT Composition for modulating muscle cell and tissue contractility for treating atherosclerosis, asthma, hypertension, glaucoma, impotence, comprising domains from urokinase-type plasminogen activator -

PT Claim 29; Fig 1Q; 117pp; English.

XX The invention relates to a composition comprising one or more domains of urokinase-type plasminogen activator (uPA). The composition is used to modulate the contractility and angiogenic activity of a mammalian muscle, endothelial cell or tissue. The composition is used for treating stroke, hypotension, hypertension, atherosclerosis, heart attack, microvascular

OS	epidermal growth factor domain; deletion; thrombolysis; fibrinolysis; ds.
XX	Homo sapiens.
SYNTHETIC.	
XX	
FH	Location/Qualifiers
FT	1..1170
Key	/*tag= a
CDS	/product= deltaE1E2-PUK
FT	/transl_except= pos:463..465, aa:Thr
FT	/note= "encodes human PUK lacking loops 1 and 2
FT	30..31
FT	/*tag= b
mutation	/note= "codons 11-32 have been deleted from between these positions"
XX	
PN	EP398361-A.
XX	
PD	22-NOV-1990.
XX	18-MAY-1990; 90EP-0109472.
PF	
XX	22-FEB-1990; 90JP-0042020.
PR	18-MAY-1989; 89JP-0126433.
PR	03-JUL-1986; 86JP-0156936.
PR	18-FEB-1987; 87JP-0036495.
PR	18-MAY-1989; 89JP-0126434.
XX	
PA	(GREC) GREEN CROSS CORP.
XX	
PI	Airmura H, Amatsuji Y, Hirose M, Kasai S, Kawabe H;
PI	Morita M, Tanabe T;
XX	
DR	WPI; 1990-350146/47.
DR	P-PSDB; AAW13636.
XX	
PT	Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent
PT	
XX	
PS	Claim 7; Page - ; 22pp; English.
XX	
CC	New variants of human prourokinase (hPUK) comprise a hPUK deficient in (1) at least part of the first loop region of the epidermal growth factor (EGF) domain; (ii) at least part of the first loop and at least part of the second loop; or (iii) at least part of the third loop. The hPUK variants show an increased blood half-life comparable to that of the whole EGF domain-deficient hPUK variant and urokinase while retaining the same properties as those of hPUK. They have potent thrombolytic activity and very little tendency to cause spontaneous bleeding. The present sequence encodes a specific variant of hPUK which lacks loops 1 and 2 of the EGF domain; the sequence does not appear in the specification and has been created using the wild-type coding sequence and the junction sequence after deletion, both of which are given (in Fig 1 and on page 8, respectively).
CC	
SQ	Sequence 1170 BP; 299 A; 326 C; 306 G; 239 T; 0 other;
XX	
Query Match	99.4%; Score 256.4; DB 11; Length 1170;
Best Local Similarity	99.6%; Pred. No. 9.4e-35;
Matches	257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG
QY	61 GGCGGGCCCTGCCCTGGAACCTGCAACTGTGCTTCAGCAAACGTACCATGCCAC 120
Db	76 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 135
QY	181 CGGAGGGACCTGGTGTATGGCAGGTGGCCTAAAGCCGCTTGTCCAAGAGTCATG 240
Db	256 CGGAGGGACCTGGTGTATGGCAGGTGGCCTAAAGCCGCTTGTCCAAGAGTCATG 315
QY	241 GTGCATGACTGCCAGAT 258
Db	316 GTGCATGACTGCCAGAT 333
RESULT	7
TD	AAT61674
XX	
DE	Human prourokinase variant lacking EGF domain loop 3, cDNA.
XX	
KW	Human; prourokinase; hPUK; variant; half-life; increase; EGF; epidermal growth factor domain; deletion; thrombolysis; fibrinolysis; ds.
KW	
XX	
OS	Homo sapiens.
OS	
SYNTHETIC.	
XX	
FH	Location/Qualifiers
FT	1..1206
Key	/*tag= a
CDS	/product= deltaE3-PUK
FT	/transl_except= pos:499..501, aa:Thr
FT	/note= "encodes human PUK lacking loop 3
FT	mutation
FT	96..97
FT	/*tag= b
FT	/note= "codons 33-42 have been deleted from between these positions"
XX	
PN	EP398361-A.
XX	
PD	22-NOV-1990.
XX	18-MAY-1990; 90EP-0109472.
PF	
XX	22-FEB-1990; 90JP-0042020.
PR	18-MAY-1989; 89JP-0126433.
PR	03-JUL-1986; 86JP-0156936.
PR	18-FEB-1987; 87JP-0036495.
PR	18-MAY-1989; 89JP-0126434.
XX	
PA	(GREC) GREEN CROSS CORP.
XX	
PI	Airmura H, Amatsuji Y, Hirose M, Kasai S, Kawabe H;
PI	Morita M, Tanabe T;
XX	
DR	WPI; 1990-350146/47.
DR	P-PSDB; AAW13637.
XX	
Human pro-urokinase variants - deficient in loop regions of epidermal growth factor, showing long blood half-life, as fibrinolytic agent	
XX	
PS	Claim 12; Page - ; 22pp; English.
XX	

CC to that of the whole EGF domain-deficient hPUK variant and urokinase
 CC while retaining the same properties as those of hPUK. They have
 CC potent thrombolytic activity and very little tendency to cause
 CC spontaneous bleeding. The present sequence encodes a specific variant
 CC of hPUK which lacks loop 3 of the EGF domain; the sequence does
 CC not appear in the specification and has been created using the
 CC wild-type coding sequence and the junction sequence after
 CC deletion, both of which are given (in Fig 1 and on page 8,
 CC respectively).
 XX

SQ sequence 1206 BP; 309 A; 334 C; 311 G; 252 T; 0 other;

Query Match 99.4%; Score 256.4; DB 11; Length 1206;
 Best Local Similarity 99.6%; Pred. No. 9.3e-35; Matches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
 Db 112 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 171

QY 61 GGCGGGCCCTGGCTGGGAACATAATTACTGCAGGAACCCAGACAAC 120
 Db 172 GGCGGGCCCTGGCTGGGAACACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 231

QY 121 AGATCTAATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 180
 Db 232 AGATCTGATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 291

QY 181 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 240
 Db 292 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 351

QY 241 GTGCATGACTGGCAGAT 258
 Db 352 GTGCATGACTGGCAGAT 369

RESULT ^ 8

AD27080 ID AAD27080 standard; DNA; 1212 BP.

XX AC AAD27080;
 XX DT 09-APR-2002 (first entry)

DE Human urokinase-type plasminogen activator scuPA delta136-143 mutant DNA.

XX Human; urokinase-type Plasminogen activator; uPA; therapy; hypertension;
 KW stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
 KW microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
 KW tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
 KW clotting disorder; uterine contraction disorder; respiratory disease;
 KW male impotence; adult respiratory distress syndrome; scuPA delta136-143;
 KW single chain urokinase; mutant; ds.
 XX OS Homo sapiens.

Query Match 99.4%; Score 256.4; DB 24; Length 1212;
 Best Local Similarity 99.6%; Pred. No. 9.3e-35; Matches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
 Db 142 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 201

QY 61 GGCGGGCCCTGGCTGGCAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 120
 Db 202 GGCGGGCCCTGGCTGGCAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 261

QY 121 AGATCTAATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 180
 Db 262 AGATCTGATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 321

QY 181 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 240
 Db 322 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 381

QY 241 GTGCATGACTGGCAGAT 258
 Db 382 GTGCATGACTGGCAGAT 399

RESULT ^ 9

AD61671 ID AAT61671 standard; cDNA; 1236 BP.

XX AC AAT61671;
 XX DT 04-JUN-1997 (first entry)

DE Human native prourokinase cDNA.

XX Human; prourokinase; hPUK; variant; half-life; increase; EGF;
 KW epidermal growth factor domain; deletion; thrombolysis;
 KW fibrinolysis; ds.
 XX OS Homo sapiens.

XX WO200197752-A2.

FT PD 27-DEC-2001.

XX PR 13-JUN-2001; 2001WO-US18976.

XX PR 20-JUN-2000; 2000US-212874P.

XX

PA (UYPE-) UNIV PENNSYLVANIA.
 XX Cines DB, Higazi AA;
 XX WPI; 2002-122240/16.
 DR P-PSDB; AAE16547.

PT Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 PT comprising domains from urokinase-type plasminogen activator -

XX PS Claim 29; Fig 10; 117pp; English.

XX The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
 CC disorders, thrombotic microangiopathies, surgically induced thrombotic
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is a DNA encoding human urokinase-type plasminogen activator
 CC (uPA) single chain urokinase (scuPA) deletion mutant designated as
 CC scuPA delta136-143.

XX SQ Sequence 1212 BP; 313 A; 333 C; 313 G; 253 T; 0 other;

Query Match 99.4%; Score 256.4; DB 24; Length 1212;
 Best Local Similarity 99.6%; Pred. No. 9.3e-35; Matches 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
 Db 142 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 201

QY 61 GGCGGGCCCTGGCTGGCAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 120
 Db 202 GGCGGGCCCTGGCTGGCAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 261

QY 121 AGATCTAATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 180
 Db 262 AGATCTGATGCTCTTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 321

QY 181 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 240
 Db 322 CGGAGGCCACCTGGTGCATGTGCAGGTGGGCTAAAGCCCTGTCAAGAGTCATG 381

QY 241 GTGCATGACTGGCAGAT 258
 Db 382 GTGCATGACTGGCAGAT 399

Db	322 CGGAGGGGACCCCTGGTGCATATGTCAGGTGGCCTAAAGCCGCTTGTCCAAGAGTCATG 381	Db	322 CGGAGGGGACCCCTGGTGCATATGTCAGGTGGCCTAAAGCCGCTTGTCCAAGAGTCATG 381
QY	241 GTGCATGACTGCCAGAT 258	QY	241 GTGCATGACTGCCAGAT 258
Db	382 GTGCATGACTGCCAGAT 399	Db	382 GTGCATGACTGCCAGAT 399
RESULT 11		RESULT 12	
AAQ06133		AAQ06134	
ID AAQ06133 standard; DNA; 1236 BP.		ID AAQ06134 standard; DNA; 1236 BP.	
XX		XX	
AC AAQ06133;		AC AAQ06134;	
XX		XX	
DT 21-FEB-1991 (first entry)		DT 21-FEB-1991 (first entry)	
DE Sequence encoding human pro-urokinase variant.		DE Sequence encoding human pro-urokinase variant.	
XX		XX	
KW Thrombin; fibrin; bleeding; PHR22; ds.		KW Thrombin; fibrin; bleeding; PHR24; ds.	
XX		XX	
OS Homo sapiens.		OS Homo sapiens.	
XX		XX	
FH Key Location/Qualifiers		FH Key Location/Qualifiers	
FT CDS 1..1233		FT CDS 1..1233	
FT /*tag= a		FT /*tag= a	
PN EP398362-A.		PN EP398362-A.	
XX		XX	
PD 22-NOV-1990.		PD 22-NOV-1990.	
XX		XX	
PF 18-MAY-1990; 90EP-0109473.		PF 18-MAY-1990; 90EP-0109473.	
XX		XX	
PR 18-MAY-1989; 89JP-0126434.		PR 18-MAY-1989; 89JP-0126434.	
XX		XX	
PA (GREC) GREEN CROSS CORP.		PA (GREC) GREEN CROSS CORP.	
XX		XX	
PI Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M;		PI Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M;	
PT Kawabe H, Arimura H;		PT Kawabe H, Arimura H;	
XX		XX	
DR WPI; 1990-350147/47.		DR WPI; 1990-350147/47.	
DR P-PSDB; AAR07902.		DR P-PSDB; AAR07902.	
XX		XX	
PT Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.		PT Human pro-urokinase variant - produced by recombinant methods, showing increased half life in blood and high affinity for fibrin.	
XX		XX	
PS Disclosure: Fig 1; 27pp; English.		PS Disclosure: Fig 1; 27pp; English.	
XX		XX	
CC Modified pro-urokinase has a longer half-life in blood, and dissolves		CC Modified pro-urokinase has a longer half-life in blood, and dissolves	
CC thrombin without causing the spontaneous bleeding associated with		CC thrombin without causing the spontaneous bleeding associated with	
CC urokinase. The modification puts an epidermal growth factor domain		CC urokinase. The modification puts an epidermal growth factor domain	
CC into the protein, containing the sequence Asn-X-Ser or Asn-X-Thr		CC into the protein, containing the sequence Asn-X-Ser or Asn-X-Thr	
CC where X is any residue.		CC where X is any residue.	
CC Plasmid PHR22 is disclosed as containing the modified sequence.		CC Plasmid PHR24 is disclosed as containing the modified sequence.	
XX		XX	
SQ Sequence 1236 BP; 317 A; 343 C; 319 G; 257 T; 0 other;		SQ Sequence 1236 BP; 318 A; 343 C; 319 G; 256 T; 0 other;	
Query Match 99.4%; Score 256.4; DB 11; Length 1236;		Query Match 99.4%; Score 256.4; DB 11; Length 1236;	
Best Local Similarity 99.6%; Pred. No. 9.2e-35; Indels 0; Gaps 0; Mismatches 257; Conservative 0; Mis		Best Local Similarity 99.6%; Pred. No. 9.2e-35; Indels 0; Gaps 0; Mismatches 257; Conservative 0; Mis	
QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCACTGACACATG 60		QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCACTGACACATG 60	
Db 142 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCACTGACACATG 201		Db 142 AAAACCTGCTATGAGGGAAATGGTCACCTAACCGAGGAAGGCCAGCACTGACACATG 201	
QY 61 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAACGTACCATGCCAC 120		QY 61 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAACGTACCATGCCAC 120	
Db 202 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAACGTACCATGCCAC 261		Db 202 GGCGGGCCCTGGCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAACGTACCATGCCAC 261	
QY 121 AGATCTAATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGAAC 180		QY 121 AGATCTAATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGAAC 180	
Db 262 AGATCTGATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGAAC 321		Db 262 AGATCTGATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGAAC 321	
QY 181 CGGAGGGACCCCTGGTCTATGTCAGGTGGCCTAAGCCGCTTGTCCAAGAGTCATG 240		QY 181 CGGAGGGACCCCTGGTCTATGTCAGGTGGCCTAAGCCGCTTGTCCAAGAGTCATG 240	

Qy	241	GTGCATGACTGCCAGAT	258	Db	322	CGGAGGCCCTGGCTATGTCAGGTGGCTAAAGCCGCTGTCCAAGAGTGCATG	381
Qy	382	GTGCATGACTGCCAGAT	399	Db	382	GTGCATGACTGCCAGAT	399
RESULT 13				RESULT 14			
AAQ06135				AAQ10169			
ID	AAQ06135	standard; DNA; 1236 BP.		ID	AAQ10169	standard; DNA; 1236 BP.	
XX				XX			
AC	AAQ06135;			AC	AAQ10169;		
XX				XX			
DT	21-FEB-1991	(first entry)		DT	18-MAR-1991	(first entry)	
XX				XX			
DE	Sequence encoding human pro-urokinase variant.			DE	Encodes Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).		
XX				XX			
KW	Thrombin; fibrin; bleeding; pHR27; ds.			KW	pro-urokinase; UK-T4; plasminogen activator; myocardial infarction; cerebral thrombosis; ss.		
XX				XX			
OS	Homo sapiens.			OS	Homo sapiens.		
XX				XX			
FH	Key	Location/Qualifiers		FH	Key	Location/Qualifiers	
FT	CDS	1..1233		FT	CDS	1..1236	
FT		/*tag= a		FT		/*tag= a	
XX				FT		/product= UK-T4	
PN	EP398362-A.			XX			
XX				PN	EP405285-A.		
PD	22-NOV-1990.			XX			
XX				PD	02-JAN-1991.		
PF	18-MAY-1990;	90EP-0109473.		XX			
XX				PF	18-JUN-1990;	90EP-0111471.	
PA	(GREC) GREEN CROSS CORP.			XX			
XX				PR	19-JUN-1989;	89JP-0156302.	
PI	Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M;			XX			
PI	Kawabe H, Arimura H;			PA	(KYOW) KYOWA HAKKO KOGYO KK.		
XX				XX			
DR	WPI; 1990-350147/47.			PA	Yasamura S, Nishi T, Ito S;		
DR	P-PSDB; AAR07904.			XX			
XX				DR	WPI; 1991-008678/02.		
PT	Human pro-urokinase variant - produced by recombinant methods'			DR	P-PSDB; AAR10057.		
CC	PT showing increased half life in blood and high affinity for fibrin.			XX			
CC				PS			
CC	PS Disclosure; Fig 1; 27pp; English.			XX			
CC				PS			
CC	CC			PS			
CC	CC	Modified pro-urokinase has a longer half-life in blood, and dissolves		PS			
CC	CC	thrombin without causing the spontaneous bleeding associated with		PS			
CC	CC	urokinase. The modification puts an epidermal growth factor domain		PS			
CC	CC	into the protein, containing the sequence Asn-X-Ser or Asn-X-Thr		PS			
CC	CC	where X is any residue.		PS			
CC	CC	Plasmid pHR27 is disclosed as containing the modified sequence.		PS			
CC	CC	Sequence 1236 BP; 317 A; 342 C; 319 G; 258 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 11; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
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CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
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CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
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CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
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CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
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CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC	Sequence 1236 BP; 321 A; 338 C; 318 G; 259 T; 0 other;		PS			
CC	CC	Query Match 99.4%; score 256.4; DB 12; Length 1236;		PS			
CC	CC	Best Local Similarity 99.6%; Pred. No. 9.2e-35; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		PS			
CC	CC	DB 142 AACCTGCTATGAGGAAATGGCACTTTACCGAGGAAGGCCAGCAGACCATG 201		PS			
CC	CC</						

		Matches	257;	conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Db	202	GGCCGGCCCTGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC	261								
QY	121	AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC	180								
CC											
CC	262	AGATCTGATGCCTTCAGCTGGGCTGGGAACATAATTACTGCAGGAACCCAGACAAC	321								
Db	142	AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACCATG	201								
QY	181	CGGAGGCACCTGGTCTATGTGCAAGGTGGCTTAAGCGCTGTCCAAAGAGTCATG	240								
CC											
CC	322	CGGAGGCACCTGGTCTATGTGCAAGGTGGCTTAAGCGCTGTCCAAAGAGTCATG	381								
Db	202	GGCCGGCCCTGCCCTGGGAACCTCTGCCACTGTCTCAGCAAACGTACCATGCCAC	261								
QY	121	AGATCTAATGCTCTCAGCTGGGCTGGGAAACATAATTACTGCAGGAACCCAGACAAC	180								
CC											
Db	262	AGATCTGATGCCTTCAGCTGGGCTGGGAACATAATTACTGCAGGAACCCAGACAAC	321								
QY	1	AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAACCCAGACAAC	60								
Db	142	AAAACCTGCTATGAGGGAAATGGTCACTTACCGAGGAAGGCCAGCACCATG	201								
QY	61	GGCCGGCCCTGCCCTGGACTCTGCCACTGTCTCTAGCAAACGTACCATGCCAC	120								
Db	202	GGCCGGCCCTGCCCTGGGAACCTCTGCCACTGTCTCAGCAAACGTACCATGCCAC	261								
QY	241	GTGCATGACTGCCAGAT	258								
Db	382	GTGCATGACTGCCAGAT	399								
RESULT	15										
ID	AAQ10170	standard; DNA; 1236 bp.									
XX	AAQ10170;										
XX	18-MAR-1991	(first entry)									
XX	DE	Encodes Pro-urokinase derivative UK-S3 with Asn(153) and Thr(155).									
XX	KW	pro-urokinase; UK-S3; plasminogen activator; myocardial infarction;									
XX	KW	cerebral thrombosis; ss.									
OS	Homo sapiens.										
XX	Key	Location/Qualifiers									
FT	CDS	1..1236									
FT		/*tag= a									
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XX	EP405285-A.										
XX	PD	02-JAN-1991.									
XX	PF	18-JUN-1990;	90EP-0111471.								
XX	PR	19-JUN-1989;	89JP-0156302.								
XX	PA	(KYOW) KYOWA HAKKO KOGYO KK.									
XX	PI	Yasamura S, Nishi T, Ito S;									
XX	XX	WPI; 1991-008678/02.									
DR	DR	P-PSDB; AAR10058.									
XX	PT	New plasminogen activator almost identical to natural pro:urokinase - is thrombin resistant and used for prophylaxis, treatment of cerebral thrombosis or myocardial infarction									
XX	PS	Disclosure; Page 9; 84pp; English.									
XX	CC	UK-S3 is one example of a plasminogen activator which differs from natural human pro-urokinase at positions 153 and 155. There are corresponding codon changes at position 457-459 (Leu substituted by Asn) and at position 463 to 465 (Pro substituted by Thr) of this DNA sequence, relative to the wild-type coding region. phpa2, constructed from puk1, is cleaved with EcoRI and HindIII and a 3.4kb DNA fragment is obtained. puk1 is cleaved with HindIII and CfrI to give a 0.75kb fragment. The two fragments, together with two phosphorylated synthetic DNAs for site-specific mutation, were ligated together in the presence of T4 ligase to give puk-S3 which has the sequence given here. See also AAQ10168 and AAQ10169.									
SQ	Sequence	1236 BP; 322 A; 338 C; 317 G; 259 T; 0 other;									
Query	Match	99.4%	Score	256.4;	DB	12;	Length	1236;			
Best	Local	Similarity	99.6%	Pred.	No.	9.2e-35;					

Search completed: November 11, 2002, 11:40:39
Job time : 234 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 11, 2002, 11:36:36 ; Search time 44 Seconds
(without alignments)
2080.333 Million cell updates/sec

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Perfect score: 258
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 320260 seqs, 177392727 residues
Total number of hits satisfying chosen parameters: 640520
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/us06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/us07_NEW_PUB.seq:*

5: /cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/us09_NEW_PUB.seq:*

10: /cgn2_6/ptodata/1/pubpna/us09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/us10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/1/pubpna/us10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/us60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/1/pubpna/us60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	256.4	99.4	264	10	US-09-880-503-10
2	256.4	99.4	288	10	US-09-880-503-18
3	256.4	99.4	405	10	US-09-880-503-13
4	256.4	99.4	423	10	US-09-984-186-11
5	256.4	99.4	429	10	US-09-880-503-17
6	256.4	99.4	1212	10	US-09-880-503-15
7	256.4	99.4	1236	10	US-09-880-503-12
8	256.4	99.4	1475	10	US-09-735-705-122
9	256.4	99.4	1475	10	US-09-850-16A-122
10	256.4	99.4	1475	10	US-09-897-778-122
11	256.4	99.4	2294	10	US-09-735-705-123
12	256.4	99.4	2294	10	US-09-850-716A-123
13	256.4	99.4	2294	10	US-09-897-778-123
14	70.8	27.4	2036	10	US-09-954-456-552
15	70.8	27.4	2036	10	US-09-880-107-1612
16	65	25.2	1689	10	US-09-969-271-6
17	65	25.2	2519	10	US-09-969-271-5
18	63.4	24.6	2641	9	US-09-974-298-144
19	55.2	21.4	1683	10	US-09-912-559-1

ALIGNMENTS

RESULT 1
US-09-880-503-10
Sequence 10, Application US/09880503
Patent NO. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880, 503
CURRENT FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: US 60/212, 847
PRIORITY FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 264
TYPE: DNA
ORGANISM: Homo sapiens
US-09-880-503-10

Query Match 99.4%; Score 256.4; DB 10; Length 264;
Best Local Similarity 99.6%; Pred. No. 4e-77;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG
Db 1 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG

QY 61 GGCCGGCCCTGCCCTGGACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
Db 61 GGCCGGCCCTGCCCTGGACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120

QY 121 AGATCTATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180
Db 121 AGATCTATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180

QY 181 CGGAGGGGACCCCTGGTGTCTATGTCAGGTGGGCTAAAGCCGCTTGTCCAAGAGTGCATG 240
Db 181 CGGAGGGGACCCCTGGTGTCTATGTCAGGTGGGCTAAAGCCGCTTGTCCAAGAGTGCATG 240

QY 241 GTGCATGACTGCCAGAT 258
 |||||||
 Db 241 GTGCATGACTGCCAGAT 258

RESULT 2
 US-09-880-503-18
 ; Sequence 18, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880, 503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212, 847
 ; PRIORITY FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 18
 ; LENGTH: 288
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-18

Query Match 99.4%; Score 256.4; DB 10; Length 405;
 Best Local Similarity 99.6%; Pred. No. 4.8e-77;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCCATG 60
 |||||||
 Db 142 AAAACCTGCTATGGGGAAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 201
 ;
 QY 61 GGCCGGCCCTGCCTGGGAACTCTGCCACTGTGCTTCAGCAAACGTACCATGCCAC 120
 |||||||
 Db 202 GGCCGGCCCTGCCTGGGAACTCTGCCACTGTGCTTCAGCAAACGTACCATGCCAC 261
 ;
 QY 121 AGATCTAATGCTCTTCAGCTGGCCTGGGAACATATAATTACTGCAGGAACCCAGAC 180
 |||||||
 Db 262 AGATCTGATGCTCTTCAGCTGGCCTGGGAACATATAATTACTGCAGGAACCCAGACAC 321
 ;
 QY 181 CGGAGGCCACCTGGTCACTGTGCAGGTGGCCTAAAGCCGCTTGCTCAAGAGTGCATG 240
 |||||||
 Db 322 CGGAGGCCACCTGGTCACTGTGCAGGTGGCCTAAAGCCGCTTGCTCAAGAGTGCATG 381
 ;
 QY 241 GTGCATGACTGCCAGAT 258
 |||||||
 Db 382 GTGCATGACTGCCAGAT 399

RESULT 4
 US-09-984-186-11
 ; Sequence 11, Application US/09984186
 ; Patent No. US2002015101A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleer, Reinhard
 ; Fournier, Alain
 ; Guittion, Jean-Dominique
 ; Yeh, Patrice
 ; Jung, Gerard
 ; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rhone-poulenc Rorer Inc.
 ; STREET: 500 Arcola Road, 3C43
 ; CITY: Collegeville
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19426
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Macintosh
 ; OPERATING SYSTEM: System 7.1
 ; SOFTWARE: Word 5.1 (PatentIn)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/984, 186
 ; FILING DATE: 29-Oct-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/797, 689
 ; FILING DATE: 31-JAN-1997
 ; APPLICATION NUMBER: US 08/256, 927
 ; FILING DATE: 28-JUL-1994
 ; APPLICATION NUMBER: FR 92/01064
 ; FILING DATE: 31-JAN-1992
 ; APPLICATION NUMBER: PCT/FR93/00085
 ; FILING DATE: 28-JAN-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Smith, Ph. D., Julie K.
 ; REGISTRATION NUMBER: P-38, 619
 ; REFERENCE/DOCKET NUMBER: ST92006-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 454-3839
 ; FAX: (610) 454-3808
 ; INFORMATION FOR SEQ ID NO: 11:
 ; US-09-880-503-13

RESULT 3
 US-09-880-503-13
 ; Sequence 13, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880, 503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIORITY APPLICATION NUMBER: US 60/212, 847
 ; PRIORITY FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 13
 ; LENGTH: 405
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-13

SEQUENCE CHARACTERISTICS:
 LENGTH: 423 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA

FEATURE:
 NAME/KEY: CDS
 LOCATION: 3..419
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:
 US-09-984-186-11

Query Match 99.4%; Score 256.4; DB 10; Length 423;
 Best Local Similarity 99.6%; Pred. No. 4.9e-77; Mismatches 0;
 Matches 257; Conservative 0; Indels 0; Gaps 0;

Qy 1 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCAGACCATG 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 153 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCAGACCATG 212
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 61 GGCGGGCCCTGCGCTGGAAACTCTGCCACTGTGCCTTCAGCAACGTACCATGCCAC 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 213 GGCGGGCCCTGCGCTGGCGCTGGAAACTCTGCCACTGTGCCTTCAGCAACGTACCATGCCAC 272
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 121 AGATCTAATGCTCTCAGCTGGGCCAGAACATAATTACTGCAGAACCCAGAAC 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 273 AGATCTGATGCTCTCAGCTGGCGCTGGAAACATAATTACTGCAGAACCCAGAAC 332
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 181 CGGAGGGGACCCCTGGTGTATGTCAGGAAACCTAAAGCCGCTTGTCCAAAGAGTGCATG 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 333 CGGAGGGGACCCCTGGTGTATGTCAGGAAACCTAAAGCCGCTTGTCCAAAGAGTGCATG 392
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy - 241 GTGCATGACTGCCAGAT 258
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 393 GTGCATGACTGCCAGAT 410
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

RESULT 5
 US-09-880-503-17
 ; Sequence 17, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880,503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212, 847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-15

Query Match 99.4%; Score 256.4; DB 10; Length 1212;
 Best Local Similarity 99.6%; Pred. No. 7.9e-77; Mismatches 0;
 Matches 257; Conservative 0; Indels 1; Gaps 0; Gaps 0;

Qy 1 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCAGACCATG 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 142 AAAACCTGCTATGAGGGAAATGGTCACTTAACCGAGGAAGGCCAGCAGACCATG 201
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 61 GGCGGGCCCTGCGCTGGAACTCTGCCACTGTGCCTTCAGCAACGTACCATGCCAC 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 202 GGCGGGCCCTGCGCTGGCGCTGGAACTCTGCCACTGTGCCTTCAGCAACGTACCATGCCAC 261
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 121 AGATCTAATGCTCTCAGCTGGGCCAGAACATAATTACTGCAGAACCCAGAAC 180
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 262 AGATCTGATGCTCTCAGCTGGGCCAGAACATAATTACTGCAGAACCCAGAAC 321
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Qy 181 CGGAGGGGACCCCTGGTGTATGTCAGGAAACCTAAAGCCGCTTGTCCAAAGAGTGCATG 240
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 322 CGGAGGGGACCCCTGGTGTATGTCAGGAAACCTAAAGCCGCTTGTCCAAAGAGTGCATG 381
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 Qy 241 GTGCATGACTGCCAGAT 258
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 382 GTGCATGACTGCCAGAT 399
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 ; US-09-880-503-17

RESULT 7
 US-09-880-503-12
 ; Sequence 12, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; APPLICANT: HIGAZI, Abd Al-Roof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880,503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212, 847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1236
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-880-503-12

Query Match 99.4%; Score 256.4; DB 10; Length 1236;
Best Local Similarity 99.6%; Pred. No. 7.9e-77; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAACCTGATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 60
Db 282 AAAACCTGATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 341
QY 61 GGCGGGCCCTGCCTGGCTAAGCCGCTTGTCCAAAGAGTGATG 120
Db 342 GGCGGGCCCTGCCTGGCTAAGCCGCTTGTCCAAAGAGTGATG 401

RESULT 8
US-09-735-705-122
; Sequence 122, Application US/09850716A
; Patent No. US20020115139A1

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 122
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-850-716A-122

Query Match 99.4%; Score 256.4; DB 10; Length 1475;
Best Local Similarity 99.6%; Pred. No. 8.6e-77; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 60
Db 282 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 341
QY 61 GGCGGGCCCTGCCTGGCTAAGCCGCTTGTCCAAAGAGTGATG 120
Db 342 GGCGGGCCCTGCCTGGCTAAGCCGCTTGTCCAAAGAGTGATG 401

RESULT 9
US-09-850-716A-122
; Sequence 122, Application US/09850716A
; Patent No. US20020115139A1

; GENERAL INFORMATION:
; APPLICANT: Rettter, Marc W.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 122
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-850-716A-122

Query Match 99.4%; Score 256.4; DB 10; Length 1475;
Best Local Similarity 99.6%; Pred. No. 8.6e-77; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAACCTGCTATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 60
Db 402 AGATCTGATGCTCTTCAGCTGGCCTGGGAACATTAATTACTGCAGGAACCCAGAC 461
QY 181 CGGAGGGGACCCCTGGTCTATGTGCAGGGGGCTAAAGCCGCTTGTCCAAAGAGTGATG 240
Db 462 CGGAGGGGACCCCTGGTCTATGTGCAGGGGGCTAAAGCCGCTTGTCCAAAGAGTGATG 521
QY 241 GTGCATGACTGCGCAGAT 258
Db 522 GTGCATGACTGCGCAGAT 539

RESULT 10
US-09-897-778-122
; Sequence 122, Application US/09897778
; Patent No. US20020147143A1

; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.

Query Match 99.4%; Score 256.4; DB 10; Length 1475;
Best Local Similarity 99.6%; Pred. No. 8.6e-77; Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAACCTGATGAGGGAAATGGTCACTTTACCGAGGAAGGCCAGCAAC 60
Db 462 CGGAGGGGACCCCTGGTCTATGTGCAGGGGGCTAAAGCCGCTTGTCCAAAGAGTGATG 521
QY 241 GTGCATGACTGCGCAGAT 258
Db 522 GTGCATGACTGCGCAGAT 539

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; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 122
; LENGTH: 1475
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-897-778-122

Query Match 99.4%; Score 256.4; DB 10; Length 1475;
Best Local Similarity 99.6%; Pred. No. 8.6e-77;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
Db 282 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 341
Qy 61 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
Db 342 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 401
Qy 121 AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 60
Db 402 AGATCTGATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 461
Qy 181 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 240
Db 462 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 521
Qy 241 GTGCATGACTGCCAGAT 258
Db 522 GTGCATGACTGCCAGAT 539

RESULT 11
US-09-735-705-123

; Sequence 123, Application US/09735705
; Patent No. US2002052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-850-716A-123

Query Match 99.4%; Score 256.4; DB 10; Length 2294;
Best Local Similarity 99.6%; Pred. No. 1e-76;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
Db 268 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 327
Qy 61 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
Db 328 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 387
Qy 121 AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180
Db 388 AGATCTGATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 447
Qy 181 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 240
Db 448 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 507
Qy 241 GTGCATGACTGCCAGAT 258
Db 508 GTGCATGACTGCCAGAT 525

RESULT 12
US-09-850-716A-123

; Sequence 123, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 123
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-850-716A-123

Query Match 99.4%; Score 256.4; DB 10; Length 2294;
Best Local Similarity 99.6%; Pred. No. 1e-76;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
Db 268 AAAACCTGCTATGAGGGGAATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 327
Qy 61 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
Db 328 GGCGGGCCCTGCCCTGGAAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 387
Qy 121 AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180
Db 388 AGATCTGATGCTCTCAGCTGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 447
Qy 181 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 240
Db 448 CGGAGGCACCCCTGGCTATGTCCAGGTGGGCCAAAGCCAGACATG 507
Qy 241 GTGCATGACTGCCAGAT 258
Db 508 GTGCATGACTGCCAGAT 525

RESULT 13
US-09-897-778-123

; Sequence 123, Application US/09897778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong

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Query Match 99.4%; Score 256.4; DB 10; Length 2294;
Best Local Similarity 99.6%; Pred. No. 1e-76;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 123
; LENGTH: 2294
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-897-778-123

Query Match 99.4%; Score 256.4; DB 10; Length 2294;
Best Local Similarity 99.6%; Pred. No. 1e-76;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCCACTGACACCATG 60
Db 268 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCCACTGACACCATG 327
QY 61 GCCCGGCCCTGGCTGGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 120
Db 328 GCCCGGCCCTGGCTGGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 387
QY 121 AGATCTAATGCTCTCAGCTGGCCTGGGAACATATAATTACTGCAGGAACCCAGAAC 180
Db 388 AGATCTGATGCTCTCAGCTGGCCTGGGAACATATAATTACTGCAGGAACCCAGAAC 447

QY 181 CGGAGGCCACCTGGTGTATGTCAGGTTGGCCTAAAGCCGTTGTCAGAGTCATG 240
Db 448 CGGAGGCCACCTGGTGTATGTCAGGTTGGCCTAAAGCCGTTGTCAGAGTCATG 507

QY 241 GTGCATGACTGGCAGAT 258
Db 508 GTGCATGACTGGCAGAT 525

RESULT 14
US-09-954-456-552
; Sequence 552, Application US/09954456
; Patent No. US2002115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: US/50/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 552
; LENGTH: 2036
; TYPE: DNA
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; US-09-954-456-552

Query Match 27.4%; Score 70.8; DB 10; Length 2036;
Best Local Similarity 55.2%; Pred. No. 3.4e-14;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 6 CTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCCACTGACACCATGGCCG 65
Db 858 CTGCTATGAGGGGAACGGCAGCTGGGTACCGTGGCCAGCACCTCAGCTCGGGCC 917
QY 66 GCCCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAAACGTACCATGCCACAGATC 125
Db 918 CAGCTGGCTGGCTTGAACCTCCATGAGGAAGGCCAGCCACTGACACCATGGCCG 977
QY 126 TAATGCTCTCAGCTGGCCTGGGAACATATAATTACTGCAGGAACCCAGAAC 185
Db 978 CGCCCGGCCCTGCTGGCCCTGGGCCATGCGCTACTGCCGAATCCGGACATGACCA 1037
QY 186 GCGACCTCTGGTGTATGTCAGGTTGGCCTAAAGCCGTTGTCAGAGTCATGGTCA 245
Db 1038 GAGGCCTCTGGCTACGGTGGTAAGGACAGCCAGCGCCTCTGGAGTACTGCCCTGGA 1097
QY 246 TGACTGGCA 255
Db 1098 GGCCTGCGAA 1107

RESULT 15
US-09-880-107-1612
; Sequence 1612, Application US/09880107
; Patent No. US2002142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1612
; LENGTH: 2036
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Genbank Accession No. US2002142981A1 D14012

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Best Local Similarity 55.2%; Pred. No. 3.4e-14;
Matches 138; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
QY 6 CTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCCACTGACACCATGGCCG 65
Db 858 CTGCTATGAGGGGAACGGCAGCTGGGTACCGTGGCCAGCACCTCAGCTCGGGCC 917
QY 66 GCCCTGCCCTGGAACTCTGCCACTGGCCTTCAGCAAACGTACCATGCCACAGATC 125

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Db	978	CGCCCGGGCCCTGCTGG	CCTGGGCCCCATGCCT	ACTGCCGAATCCGG	ACAATGACGA	1037	
Qy	186	GCGACCCCTGGTGC	TATGTGCAGGTGGCCTAA	AGCCCTTGTC	CAAGAGTGCA	245	
Db	1038	GAGGCCCTGGTGC	TACGTGGTAAGGAC	CAGCGCC	TCTCTGGGAGTAC	CGCCCTGGGA	1097
Qy	246	TGACTGCGCA	255				
Db	1098	GGCCTGCGAA	1107				

Search completed: November 11, 2002, 12:58:35
Job time : 46 secs

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OM nucleic - nucleic search, using sw model

Run on:

November 11, 2002, 11:36:26 ; Search time 1968 seconds

(without alignments)
2123.189 Million cell updates/sec

Title: PCT-US02-27855-2

Perfect score: 258
Sequence: 1 aaaaacctgtatgagggaa.....tggtgcatgactgcgcagat 258

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_htc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vrt:
22: em_gss_fun:
23: em_gss_mam:
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25: em_gss_other:
26: em_gss_pro:
27: em_gss_rod:

RESULT 1
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LOCUS BE877476
DEFINITION 601485319F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3887620 5', mRNA sequence.

ACCESSION BE877476
VERSION BE877476.1 GI:10326252
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Cetartiodactyla; Hominidae; Homo.

1 (bases 1 to 700)
REFERENCE 1 NIH-MGC <http://mgc.ncbi.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LLAM5666 row: f column: 05
High quality sequence stop: 671.
Location/Qualifiers 1. .700

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8 256.4 99.4 932 14 BQ961887
9 256.4 99.4 963 14 BQ929215
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12 256.4 99.4 1067 14 BM920114
13 256.4 99.4 1075 12 BE742275
14 256.4 99.4 1087 12 BE897378
15 256.4 99.4 1164 12 BF568088
16 255.4 99.4 1175 9 AU135252
17 254.8 98.8 479 14 BM843656
18 254.8 98.8 602 14 BM849144
19 254.8 98.8 647 12 BE889213
20 254.8 98.8 980 14 BQ920793
21 253.8 98.4 595 14 BM853271
22 248.4 96.3 474 12 BF873834
23 245.4 95.1 718 9 AU128113
24 245.4 95.1 822 13 B1833559
25 244.4 94.7 1130 12 BG832239
26 243.8 94.5 913 14 BQ887418
27 240.6 93.3 775 13 BM048314
28 238 92.2 710 12 BG331244
29 234.4 90.9 625 12 BE880196
30 233.4 90.5 928 12 BG330224
31 232.8 90.2 803 12 BG741013
32 230.4 89.3 672 12 BG254622
33 226.8 87.9 549 14 BM848159
34 224.8 87.1 261 14 BM761640
35 221.6 85.9 1093 12 BE874867
36 220.6 85.5 1152 13 B1759308
37 203.6 78.9 952 12 BG035185
38 198.4 76.9 223 9 AA158183
39 191.6 74.3 638 10 BB666464
40 191.6 74.3 655 10 BB555211
41 165.4 64.1 337 12 BG007464
42 148.6 57.6 472 14 BM847321
43 142.4 55.2 901 14 BQ420628
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45 134.4 52.1 52.1 AL549674
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	256.4	99.4	767	12 BE877571	BE877571 601486523
3	256.4	99.4	799	9 AU131687	AU131687 AU131687
4	256.4	99.4	870	14 BQ641748	BQ641748 AGENCOURT
5	256.4	99.4	871	12 BQ748424	BQ748424 602705991
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 Best Local Similarity 99.6%; Pred. No. 4.8e-67;
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 Db 238 AGATCTGATGCTCTTCAGCTGGCCTGGGGAAACATAATTACTGCAGGAACCCAGACAC 297
 QY 181 CGGAGGGGACCCCTGGCCTATGTCAGGTGGGCCTAAAGCCGCTGTCCAAGAGTGCATG 240
 Db 298 CGGAGGGGACCCCTGGCCTATGTCAGGTGGGCCTAAAGCCGCTGTCCAAGAGTGCATG 357
 QY 241 GTGCACTGACTGCGCAGAT 258
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 BE877571
 LOCUS BE877571
 DEFINITION 601486523FL NIH_MGC_69 Homo sapiens mRNA clone IMAGE:3888964 5',
 ACCESSION BE877571
 VERSION GI:10326347
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 mRNA sequence.
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 EST.
 human.
 Homo sapiens
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 NIH-MGC http://mgc.ncbi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DBP/Gazzar
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: Llam9669 row: n column: 05
 High quality sequence stop: 710.
 Location/Qualifiers
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 /clone="IMAGE:3888964"
 /clone_1.lib="NIH_MGC_69"
 /tissue_type="large cell carcinoma, undifferentiated"
 /lab_host="DH10B (phage-resistant)"
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 /db_xref="taxon:9606"
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 /clone.lib="NT2RP3"
 /cell_type="teratocarcinoma"
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 cells after 2-weeks retinoic acid (RA) induction"
 BASE COUNT 198 a 233 c 212 g 152 t
 ORIGIN

/note="organ: lung; vector: PCMV-SPORT6; site_1: NotI;
 site_2: Sall; cloned unidirectionally. primer: Oligo dt.
 average insert size 1.1 kb. library constructed by life
 technologies."
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 ORIGIN
 Query Match 99.4%; Score 256.4; DB 12; Length 767;
 Best Local Similarity 99.6%; Pred. No. 5.1e-67;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
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 Db 348 GGCGGGCCCTGCTGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 407
 QY 121 AGATCTAATGCTCTTCAGCTGGCCTGGGGAAACATAATTACTGCAGGAACCCAGACAC 180
 Db 408 AGATCTGATGCTCTTCAGCTGGCCTGGGGAAACATAATTACTGCAGGAACCCAGACAC 467
 QY 181 CGGAGGGGACCCCTGGCTATGTCAGGTGGGCCTAAAGCCGCTGTCCAAGAGTGCATG 240
 Db 468 CGGAGGGGACCCCTGGCTATGTCAGGTGGGCCTAAAGCCGCTGTCCAAGAGTGCATG 527
 QY 241 GTGCACTGACTGCGCAGAT 258
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RESULT 3
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 sequence.
 ACCESSION AU131687
 VERSION GI:10992041
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 EST.
 human.
 Homo sapiens
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 NIH-MGC http://mgc.ncbi.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DBP/Gazzar
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: Llam9669 row: n column: 05
 High quality sequence stop: 710.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 cells after 2-weeks retinoic acid (RA) induction"
 BASE COUNT 198 a 233 c 212 g 152 t 4 others
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QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACCCATG 60
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 Db 368 GGCAGGGCCCTGCCCTGGAACTCTGCCACTGTCTTCAGCAAACGTACCATGCCAC 429
 QY 121 AGATCTAATGCTCTTCAGCTGGCCCTGGGAACATAATTACTGCAGGAACCCAGACAC 180
 Db 428 AGATCTGATGCTTCAGCTGGCCCTGGGAACATAATTACTGCAGGAACCCAGACAC 487
 QY 181 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTCCAAGAGTCATG 240
 Db 488 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTCCAAGAGTCATG 547
 QY 241 GTGCATGACTGCGCAGAT 258
 Db 548 GTGCATGACTGCGCAGAT 565

RESULT 6
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 5' mRNA sequence.
 ACCESSION BQ886981
 VERSION BQ886981.1 GI:22278995
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 913)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 595.
 Location/Qualifiers

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 /note="Organ: prostate; Vector: pOTB7; Site_1: xhol;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/xhol sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

BASE COUNT 217 a 276 c 250 g 169 t 1 others
 ORIGIN

Query Match 99.4%; Score 256.4; DB 14; Length 913;
 Best Local Similarity 99.6%; Pred. No. 5.5e-67;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACCCATG 60
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RESULT 7
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 mRNA sequence.
 ACCESSION BE742186
 VERSION BE742186.1 GI:10156178
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 930)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLMC520 row: h column: 21
 High quality sequence stop: 743.
 Location/Qualifiers
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 /db_xref="taxon:9606"
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 /lab_host="DH10B (phage-resistant)"
 /note="Organ: ovary; Vector: pOTB7; Site_1: xhol; Site_2:
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 cloned into EcoRI/xhol sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 217 a 265 c 264 g 184 t
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 Query Match 99.4%; Score 256.4; DB 12; Length 930;
 Best Local Similarity 99.6%; Pred. No. 5.6e-67;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACCCATG 60
 Db 20 AAAACCTGCTATGAGGGAAATGGTCACCTTACCGAGGAAGGCCAGCACTGACCCATG 79

QY 61 GGCCGGCCCTGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
 Db 80 GGCCGGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 139
 QY 121 AGATCTAATGCTCTCAGCTGGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 180
 Db 140 AGATCTGATGCTCTCAGCTGGGCCTGGGAAACATAATTACTGCAGGAACCCAGACAC 199
 QY 181 CGGAGGCGACCCCTGGTCTATGTGCAGGTGGCTAAAGCCCTGTCCAAGAGTCATG 240
 Db 200 CGGAGGCGACCCCTGGTCTATGTGCAGGTGGCTAAAGCCCTGTCCAAGAGTCATG 259
 QY 241 GTGCATGACTGCGCAGAT 258
 Db 260 GTGCATGACTGCGCAGAT 277

RESULT 8
 BQ961887 BQ961887 AGENCOURT_8778892 NIH_MGC_42 Homo sapiens CDNA clone IMAGE:6378687 932 bp mRNA linear EST 21-AUG-2002
 LOCUS DEFINITION 5', mRNA sequence.
 REFERENCE BQ961887
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2564 row: h column: 16
 High quality sequence stop: 606.
 Location/Qualifiers

FEATURES
 source
 1. .932
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6378687"
 /clone_1lib="NIH_MGC_42"
 /tissue-type="epithelioid carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: pancreas; Vector: pOTB7; Site_1: XbaI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library. 1" others

BASE COUNT
 ORIGIN 225 a 281 c 248 g 177 t 1 others

Query Match 99.4%; Score 256.4; DB 14; Length 932;
 Best Local Similarity 99.6%; Pred. No. 5.6e-67;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACATG 60
 Db 303 AAAACCTGCTATGAGGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACATG 362
 QY 61 GGCGGGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120

RESULT 9
 BQ929215 BQ929215 AGENCOURT_8958654 NIH_MGC_101 Homo sapiens CDNA clone IMAGE:6460542 963 bp mRNA linear EST 20-AUG-2002
 LOCUS DEFINITION 5', mRNA sequence.
 REFERENCE BQ929215
 AUTHORS NIH-MGC
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2647 row: g column: 07
 High quality sequence stop: 566.
 Location/Qualifiers

FEATURES
 source
 1. .963
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:6460542"
 /clone_1lib="NIH_MGC_101"
 /tissue-type="epidermoid carcinoma cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2: XbaI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
 NIH_MGC Library."
 BASE COUNT
 ORIGIN 221 a 301 c 256 g 182 t 3 others

Query Match 99.4%; Score 256.4; DB 14; Length 963;
 Best Local Similarity 99.6%; Pred. No. 5.7e-67;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACATG 60
 Db 277 AAAACCTGCTATGAGGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACATG 336
 QY 61 GGCGGGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 120
 Db 337 GGCGGGCCCTGCCCTGGAACTCTGCCACTGTCCCTCAGCAAACGTACCATGCCAC 396

RESULT 12
BM920114 LOCUS BM920114
DEFINITION AGENCOURT_6706522 NIH_MGC_120 Homo sapiens
5', mRNA sequence.
ACCESSION BM920114
VERSION BM920114.1 GI:19370493
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1067)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE NIH-MGC
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLIAM12780 row: d column: 20
High quality sequence stop: 754.
FEATURES
source
/organism="Homo sapiens"
'/db_xref="taxon:9606"
'/clone="IMAGE:5749987"
'/clone_lib="NIH_MGC_120"
'/lab_host="DH10B"
'/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; site_1: NotI; site_2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."
BASE COUNT 256 a 323 c 273 g 208 t 7 others
ORIGIN
Query Match 99.4%; Score 256.4; DB 14; Length 1067;
Best Local Similarity 99.6%; Pred. No. 6e-67;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 328 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG
Qy 1 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
Db 328 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 387
Qy 61 GGCGGGCCCTGCCTGGAACTCTGCCACTGTGCTCTCAGCAAACGTTACCATGCCAC 120
Db 388 GGCGGGCCCTGCCTGGAACTCTGCCACTGTGCTCTCAGCAAACGTTACCATGCCAC 447
Qy 121 AGATCTAATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 180
Db 448 AGATCTGATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 507
Qy 181 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTGTCAGAGTCATG 240
Db 508 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTGTCAGAGTCATG 567
Qy 241 GTGCATGACTGCGCAGAT 258
Db 568 GTGCATGACTGCGCAGAT 585
RESULT 13
BE742275 LOCUS BE742275
DEFINITION 601575693F1 NIH_MGC_9 Homo sapiens
mRNA sequence.
ACCESSION BE742275
VERSION BE742275.1 GI:10156267
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTB/RTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLIAM520 row: j column: 24
High quality sequence stop: 681.
FEATURES
source
/organism="Homo sapiens"
'/clone="IMAGE:3836663"
'/clone_lib="NIH_MGC_9"
'/tissue_type="adenocarcinoma cell line"
'/lab_host="DH10B (phage-resistant)"
'/note="Organ: ovary; Vector: pOTB7; site_1: xbaI; site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/xbaI sites using the following 5' adapter: GGCACGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 226 a 322 c 290 g 237 t
ORIGIN
Query Match 99.4%; Score 256.4; DB 12; Length 1075;
Best Local Similarity 99.6%; Pred. No. 6e-67;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db 20 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 79
Qy 1 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 60
Db 20 AAAACCTGCTATGAGGGGAATGGTCACCTTACCGAGGAAGGCCAGCACTGACACCATG 139
Qy 61 GGCGGGCCCTGCCTGGAACTCTGCCACTGTGCTCTCAGCAAACGTTACCATGCCAC 120
Db 80 GGCGGGCCCTGCCTGGAACTCTGCCACTGTGCTCTCAGCAAACGTTACCATGCCAC 180
Qy 121 AGATCTAATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 180
Db 140 AGATCTGATGCTCTCAGCTGGCCTGGGAACATAATTACTGCAGGAACCCAGACAAC 199
Qy 181 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTGTCAGAGTCATG 240
Db 200 CGGAGGGACCCCTGGCTATGTGCAGGTGGCCTAAAGCCGCTGTGTCAGAGTCATG 259

QY 241 GTGCATGACTGCGCAGAT 258
 Db 260 GTGCATGACTGCGCAGAT 277

RESULT 14
 LOCUS BE897378
 DEFINITION 601437369FL NIH_MGC_72 Homo sapiens mRNA sequence.
 ACCESSION BE897378
 VERSION BE897378
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1087)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabps-r@mail.nih.gov
 Tissue Procurement: ATCC/DCTD/DP
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
 Plate: LLAM9756 row: j column: 17
 High quality sequence start: 2
 High quality sequence stop: 654.
 Location/Qualifiers 1. .1087

FEATURES source
 .

FEATURES source
 .

Query Match 99.4%; Score 256.4; DB 12; Length 1087;
 Best Local Similarity 99.6%; Pred. No. 6e-67; Mismatches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
 Db 268 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 327

QY 61 GCGCGGCCCTGCTGCCACTCTGCCACTGCTCTCAGCAACGTACCATGCCAC 120
 Db 328 GCGCGGCCCTGCTGCCCTGGAACCTCTGCCACTGCTCTCAGCAACGTACCATGCCAC 387

QY 121 AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACAGGAGCACAC 180
 Db 388 AGATCTGATGCTCTCAGCTGGCCTGGGAAACATAATTACAGGAGCACAC 180

QY 181 CGGAGGCGACCCCTGGCTATGTCAGGTGGCCATAAGCCGCTGTCCAAGAGTCATG 240
 Db 448 CGGAGGCGACCCCTGGCTATGTCAGGTGGCCATAAGCCGCTGTCCAAGAGTCATG 447

QY 241 GTGCATGACTGCGCAGAT 258
 Db 508 GTGCATGACTGCGCAGAT 525

RESULT 15
 LOCUS BF568088
 DEFINITION 602184082FL NIH_MGC_42 Homo sapiens mRNA clone IMAGE:4299981 5,
 mRNA sequence.
 ACCESSION BF568088
 VERSION BF568088.1 GI:11641506
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 REFERENCE 1 (bases 1 to 1164)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabps-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
<http://image.llnl.gov>
 Plate: LLCM1158 row: c column: 22
 High quality sequence start: 727.
 Location/Qualifiers 1. .1164

FEATURES source
 .

FEATURES source
 .

Query Match 99.4%; Score 256.4; DB 12; Length 1164;
 Best Local Similarity 99.6%; Pred. No. 6.3e-67; Mismatches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 60
 Db 308 AAAACCTGCTATGAGGGATGGTCACTTTACCGAGGAAGGCCAGCACTGACACCATG 367

QY 61 GCGCGGCCCTGCTGCCACTCTGCCACTGCTCTCAGCAACGTACCATGCCAC 120
 Db 368 GCGCGGCCCTGCTGCCACTCTGCCACTGCTCTCAGCAACGTACCATGCCAC 427

QY 121 AGATCTAATGCTCTCAGCTGGCCTGGGAAACATAATTACAGGAGCACAC 180
 Db 428 AGATCTGATGCTCTCAGCTGGCCTGGGAAACATAATTACAGGAGCACAC 180

QY 181 CGGAGGCGACCCCTGGCTATGTCAGGTGGCCATAAGCCGCTGTCCAAGAGTCATG 240
 Db 488 CGGAGGCGACCCCTGGCTATGTCAGGTGGCCATAAGCCGCTGTCCAAGAGTCATG 547

QY 241 GTGCATGACTGCGCAGAT 258
 Db 548 GTGCATGACTGCGCAGAT 565